

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 24, 2004, 22:51:30 ; Search time 20 Seconds
(without alignments)
43.286 Million cell updates/sec

Title: US-09-920-480B-1
Perfect score: 40
Sequence: 1 FLDQVAFXV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing First 45 summaries

Database : PIR 7.8:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	35.0		7	2	S57274	triacetylglycerol li fatty-acid synthase
2	32.5		6	2	A20186	T-cell receptor beta adiopokinetic hormo
3	32.5		7	2	PT0569	hypertrahaloemic adiopokinetic hormo
4	32.5		8	2	A28004	adiopokinetic hormo
5	32.5		8	2	S08935	adiopokinetic hormo
6	32.5		8	2	S10596	adiopokinetic hormo
7	32.5		8	2	A49823	neuropeptide Led-C
8	32.5		8	2	A4490	adiopokinetic hormo
9	32.5		8	2	S55310	adiopokinetic hormo
10	32.5		8	2	A58620	beta-galactosidase
11	32.5		8	2	A47618	beta-galactosidase
12	32.5		9	2	D24180	beta-2-macroglobu
13	32.5		9	2	S66645	synaptosomal assoc
14	30.0		5	2	B44823	hypertrehalosemic
15	30.0		7	2	A28709	neuropeptide Led-C
16	30.0		7	2	A34818	neuropeptide Led-C
17	30.0		7	2	C56793	neuropeptide Led-C
18	30.0		7	2	PN0649	neuropeptide Led-C
19	30.0		7	2	S09066	neuropeptide Led-C
20	30.0		8	2	S08936	neuropeptide Led-C
21	30.0		8	2	B49823	neuropeptide Led-C
22	30.0		8	2	B44960	neuropeptide Led-C
23	30.0		8	2	A33950	neuropeptide Led-C
24	30.0		8	2	S11545	neuropeptide Led-C
25	30.0		8	2	E60588	neuropeptide Led-C
26	30.0		8	2	G60588	neuropeptide Led-C
27	30.0		8	2	B24749	neuropeptide Led-C
28	30.0		8	2	A23967	neuropeptide Led-C
29	30.0		8	2	S29272	neuropeptide Led-C

RESULT 1

SS57274 triacylglycerol lipase (EC 3.1.1.3) - *Psychrobacter immobilis* (fragment)

C;Species: *Psychrobacter immobilis*
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995

R;Ariigny, J.-L.; Feiller, G.; Gerday, C.

Biochim. Biophys. Acta 1263, 103, 1995

A;Title: Corrigendum to "Cloning, sequence and structural features of a lipase from the

A;Reference number: S557274; PMID:95359197; PMID:1632728

A;Accession: S57274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-7 <ARP>

C;Cross-references: EMBL:X67712

C;Keywords: carboxylic ester hydrolase

Query Match 35.0%; Score 14; DB 2; Length 7;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Mismatches 1; Indels 0; Gaps 0;

Matches 2; Conservative 1; Gaps 0;

Qy 3 DQV 5

Db 5 DQI 7

RESULT 2

A20186 fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 05-Jun-1977 #sequence_revision 05-Jun-1987 #text_change 05-May-2000

R;McCarthy, A.D.; Aitken, A.; Hardie, G.; Santikarn, S.; Williams, D.H.

FEBS Lett. 160, 295-300, 1983

A;Title: Amino acid sequence around the active serine in the acyl transferase domain of

A;Reference number: A20186; PMID:83287765; PMID:6554204

A;Accession: A20186

A;Molecule type: Protein

A;Residues: 1-6 <MCC>

C;Keywords: acyltransferase; coenzyme A

Query Match 32.5%; Score 13; DB 2; Length 6;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;

Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 1; Gaps 0;

Qy 2 LDQVA 6

Db 2 LDQVA 6

RESULT 3

PT0569

RESULT 4
 A28004
 adipokinetic hormone G - two-spotted cricket
 N: Alternative names: AKH-G
 C: Species: Gryllus bimaculatus (two-spotted cricket)
 C: Accession: A28004
 C: Sequence revision 24-Oct-1997
 R/Gaede, G.; Rinehart, K.L.
 Biochem. Biophys. Res. Commun. 149, 908-914, 1987
 A: Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide
 A: Reference number: A28004; MUID:88106553; PMID:3426616
 A: Accession: A28004
 A: Molecule type: protein
 A: Residues: 1-8 <GAE>
 A: Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C: Superfamily: adipokinetic hormone
 C: Keywords: hormone; neuropeptide; pyroglutamic acid (Gln)
 F:1/Modified site: amidated carboxyl end (Trp) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05; 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 1; Indels 0;

Qy 4 QVAF 7
 Db 1 QVNF 4

RESULT 5
 S08995
 hyperrehalosemic hormone I - oriental cockroach
 N: Alternative names: Paa-CH₂I
 C: Species: Blatta orientalis (oriental cockroach)
 C: Accession: S08995
 C: Sequence revision 24-Oct-1997
 R/Gaede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
 A: Title: Primary structures of hyperrehalosemic neuropeptides isolated from the corpora allata and of the stock insect *Extatosoma tiaratum* assigned by tandem fast atom bombardment and of the stock insect *Extatosoma tiaratum* assigned by tandem fast atom bombardment
 A: Reference number: S08995; MUID:90253659; PMID:2340112
 A: Accession: S08995
 A: Molecule type: protein
 A: Residues: 1-8 <GAE>
 A: Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C: Superfamily: adipokinetic hormone
 C: Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln)
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05; 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 1; Indels 0;

Qy 4 QVAF 7
 Db 1 QVNF 4

RESULT 6
 S10596
 adipokinetic hormone - pond skimmer
 C: Species: *Libellula auripennis*
 C: Accession: S10596
 C: Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997
 R/Gaede, G.
 Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
 A: Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone
 A: Reference number: S10596; MUID:90339055; PMID:2399213
 A: Molecule type: protein
 A: Accession: S10596
 A: Residues: 1-8 <BIO>
 C: Comment: This peptide has both adipokinetic and hyperrehalosemic activities.
 C: Superfamily: adipokinetic hormone
 C: Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
 F:1/Modified site: amidated carboxyl end (Trp) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05; 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 1; Indels 0;

Qy 4 QVAF 7
 Db 1 QVNF 4

RESULT 7
 A49823
 adipokinetic hormone I - American cockroach
 N: Alternative names: Periplaneta CC-1
 C: Species: *Periplaneta americana* (American cockroach)
 C: Accession: A49823
 C: Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
 R/Scarborough, R.M.; Janieson, G.C.; Kalish, P.; Kramer, S.J.; McEnroe, G.A.; Miller, C
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
 A: Title: Isolation and primary structure of two peptides with cardioacceleratory and hyperrehalosemic activities
 A: Reference number: A49823; MUID:84298179; PMID:6591205
 A: Molecule type: protein
 A: Accession: A49823
 A: Residues: 1-8 <SCA>
 C: Superfamily: adipokinetic hormone
 C: Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05; 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 1; Indels 0;

Qy 4 QVAF 7
 Db 1 QVNF 4

RESULT 8
 A4960
 neuropeptide Led-CC-I - Colorado potato beetle
 C: Species: *Leptinotarsa decemlineata* (Colorado potato beetle)
 C: Accession: A4960
 C: Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 R/Gaede, G.; Kellner, R.

Peptides 10, 1287-1289, 1989
 A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and C;Superfamily: adipokinetic hormone
 C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln)
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental
 A;Molecule type: protein
 A;Residues: 1-8 <GAB₂
 Query Match Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 QVAF 7
 Db 1 QVNF 4

RESULT 9
 S55310 adipokinetic hormone - damselfly (Pseudagrion inconstipatum)
 N;Alternate names: Psi-AKH
 C;Species: Pseudagrion inconstipatum
 C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
 C;Accession: S55310
 R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
 Biochem. J. 302, 539-543, 1994
 A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconstipatum
 A;Reference number: S55310; MUID:94379987; PMID:8093008
 A;Accession: S55310
 A;Molecule type: protein
 A;Residues: 1-8 <JAN₂
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental
 Query Match Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 QVAF 7
 Db 1 QVNF 4

RESULT 10
 A58620 adipokinetic hormone - damselfly (Ischnura senegalensis)
 C;Species: Ischnura senegalensis
 C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
 C;Accession: A58620
 R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
 Biochem. J. 302, 539-543, 1994
 A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconstipatum
 A;Reference number: S55310; MUID:94379987; PMID:8093008
 A;Accession: A58620
 A;Molecule type: protein
 A;Residues: 1-8 <JAN₂
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental
 Query Match Score 13; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 QVAF 7
 Db 1 QVNF 4

Qy 3 DQVAEXV 9
 Db : | :
 2 DEFPPFAL 8

RESULT 14

B44823 synaptosomal-associated protein SNAP-25 peptide 10A - rabbit (fragment)
 N;Alternate names: superprotein peptide 10A
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
 C;Accession: B44823
 R;Iewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
 J. Neurosci. 11, 3412-3421, 1991
 A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
 A;Reference number: A44823; MUID:92044785; PMID:1941090
 A;Accession: B44823
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <LOB>
 A;Experimental source: visual tissue
 A;Note: sequence extracted from NCBI backbone (NCBIP:64255)
 C;Keywords: membrane trafficking

Query Match 30.0%; Score 12; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 DQVA 6
 : |
 Db 1 EQMA 4

RESULT 15

A2B709 phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)
 C;Species: Bacillus cereus
 C;Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
 C;Accession: A2B709
 R;Olisen, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
 Biochemistry 27, 2229-2234, 1988
 A;Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidence
 A;Reference number: A2B709; MUID:88241058; PMID:3132206
 A;Accession: A2B709
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-7 <Q1S>

Query Match 30.0%; Score 12; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LDQV 5
 : |
 Db 3 IDHV 6

Search completed: February 24, 2004, 22:57:23
 Job time : 22 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
1	15	AL12	CARMA	8	1	P38499	Procambarus
2	14	AL12	CARMA	8	1	P38498	Procambarus
3	14	AL12	CARMA	8	1	P83379	Lycopersico
4	14	AL12	CARMA	8	1	P38641	mus musculu
5	13	AL12	CARMA	8	1	P81809	carcinus ma
6	13	AL12	CARMA	8	1	P81811	carcinus ma
7	13	AL12	CARMA	8	1	P81812	carcinus ma
8	13	AL12	CARMA	8	1	P81813	rattus norv
9	12	AL12	CARMA	8	1	P41872	enterococcus
10	12	AL12	CARMA	8	1	P83316	panagrellus
11	12	AL12	CARMA	8	1	P83275	macrobrachi
12	30.0	LPK2	PERAM	8	1	P38499	Procambarus
13	12	LPK2	PERAM	8	1	P38498	Procambarus
14	12	NPMB	BOVIN	9	1	P83379	Lycopersico
15	11	NPMB	BOVIN	9	1	P38641	mus musculu
16	11	NPMB	BOVIN	4	1	P81809	carcinus ma
17	11	NPMB	BOVIN	8	1	P81811	carcinus ma
18	11	NPMB	BOVIN	8	1	P81812	carcinus ma
19	11	NPMB	BOVIN	27.5	8	P21142	leucophaea
20	11	NPMB	BOVIN	8	1	P80632	zea mays (m
21	11	NPMB	BOVIN	8	1	P30087	homo sapien
22	11	NPMB	BOVIN	9	1	P82926	bos taurus
23	10	NPMB	BOVIN	27.5	9	P38640	mus musculu
24	10	NPMB	BOVIN	25.0	4	P2561	hirundo medi
25	10	NPMB	BOVIN	25.0	4	P5807	anthophleura
26	10	NPMB	BOVIN	25.0	5	P80628	zea mays (m
27	10	NPMB	BOVIN	25.0	6	P1491	locusta mig
28	10	NPMB	BOVIN	25.0	6	P42985	leptinotarsa
29	10	NPMB	BOVIN	25.0	7	P81805	carcinus ma
30	10	NPMB	BOVIN	25.0	7	P81806	carcinus ma
31	10	NPMB	BOVIN	25.0	7	P81808	carcinus ma
32	10	NPMB	BOVIN	25.0	7	P1871	helisoma tr
33	10	NPMB	BOVIN	25.0	7	P83274	macrobrachi

RT allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -!- SIMILARITY: May act as a neurotransmitter or neuromodulator.
 CC -!- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Multipeptide Family.
 SEQUENCE 7 AA;
 672879cDB476AC0 CRC64;
 Query Match 35.0%; Score 14; DB 1; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;
 QY 3 DQVAF 7
 | | |
 Db 1 DPYAF 5
 RESULT 3
 NS3_MYCTU STANDARD; PRT; 8 AA.
 ID NS3_MYCTU STANDARD; PRT; 8 AA.
 AC P8112;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB 3.0 kDa non-secretory protein 3 (Fragment).
 OS *Mycobacterium tuberculosis*.
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
 Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP
 SEQUENCE.
 RC STRAIN=H37RV;
 RA Prasad H.K., Annapurna P.S.,
 RL Submitted (DEC-1997) to Swiss-Prot.
 CC -!- CAUTION: We are unable to find this protein in the translation of
 the genome of strain H37RV.
 FT NON TER 1
 FT NON TER 8
 SEQUENCE 8 AA; 919 MW; 8D3DC40B19CDC2D2 CRC64;
 Query Match 35.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;
 QY 5 VAF 7
 | | |
 Db 2 VAF 4
 RESULT 4
 AL11_CARMA STANDARD; PRT; 9 AA.
 ID AL11_CARMA STANDARD; PRT; 9 AA.
 AC P8114;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 11.
 OS *Carcinus maenas* (Common shore crab) (Green crab).
 OC Eumalacostraca; Crustacea; Malacostraca;
 OC Eubrachyura; Portunoidea; Portunidae; *Carcinus*.
 OX NCBI_TaxID=6759;
 RN [1]
 RP
 SEQUENCE.
 RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RA Duke H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.-P.,
 Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 allatostatin superfamily in the shore crab *Carcinus maenas*";
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -!- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Amidation; Multipeptide Family.
 FT MOD RES 9 AA; 927 MW; AMIDATION.
 Query Match 35.0%; Score 14; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 1;
 QY 4 QVAF 7
 | | |
 Db 4 QVAF 7
 RESULT 5
 AKHG_GRYBI STANDARD; PRT; 8 AA.
 ID AKHG_GRYBI STANDARD; PRT; 8 AA.
 AC P14986;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adiokinetic hormone G (AKH-G) (RO II).
 OS *Gryllus bimaculatus* (Two-spotted cricket), and
 ROMalea microptera (Lubber grasshopper).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
 OC Gryllus.
 OX NCBI_TaxID=6999, 7007;
 RN [1]
 RP
 SEQUENCE.
 RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
 RX MEDLINE=8810553; PubMed=3426616;
 RA Gaede G., Rinehart K.L. Jr.;
 RL "Primary sequence analysis by fast atom bombardment mass spectrometry
 of a peptide with adipokinetic activity from the corpora cardiaca of
 the cricket *Gryllus bimaculatus*";
 RT Biochem. Biophys. Res. Commun. 149:908-914 (1987).
 RN [2]
 RP
 SEQUENCE.
 RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
 RX MEDLINE=8914502; PubMed=3226948;
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
 RL "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
 the lubber grasshopper, *Romalea microptera*";
 RT Peptides 9:681-688 (1988).
 RL [2]
 CC -!- FUNCTION: This hormone, released from cells in the corpora
 cardiaca after the beginning of flight, causes release of
 diglycerides from the fat body and then stimulates the flight
 muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / RPCH family.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 DR Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 KW PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 1 1
 FT MOD RES 0 0
 SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;
 Query Match 32.5%; Score 13; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 1;
 QY 4 QVAF 7
 | | |
 Db 1 QVNF 4
 RESULT 6
 AKH_LIBAU STANDARD; PRT; 8 AA.
 ID AKH_LIBAU
 AC P25418;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE	Adipokinetic hormone (AKH).
OS	<i>Libellula auripennis</i> (Skimmer dragonfly).
OC	Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX	
RN	[1]
RP	SEQUENCE, AND SYNTHESIS.
RC	TISSUE=Corpora cardiaca;
RX	Medline=9035055; PubMed=2390213;
RA	Gaede G.;
RT	"The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone family isolated and sequenced from a dragonfly."
RT	"This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight muscles to use these diglycerides as an energy source.
CC	-1- FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight muscles to use these diglycerides as an energy source.
CC	-1- SUBCELLULAR LOCATION: Belongs to the AKH / RPCH family.
DR	PIR; S10596; S10597.
DR	InterPro; IPR002047; AKH.
DR	Prosite; PS00256; AKH; 1.
KW	Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	MOD_RES 8 8 AMIDATION.
SQ	SEQUENCE 8 AA; 978 MW; 86654771AA0452D6 CRC64;
Qy	Query Match 32 Local Similarity 75.0% Score 13; DB 1; Length 8; Best Local Similarity 75.0% Pred. No. 1.4e+05; Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	4 QYAF 7 1 QYNF 4
RESULT 7	HTF1_PERAM STANDARD; PRT; 8 AA.
ID	P04548; Rel. 05, Created)
DT	13-AUG-1987 (Rel. 05, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DE	Hypertrachealosaeamic factor I (Neuropeptide M-I) (Periplanetin CC-I)
DE	(PeA-CH-I) (Leu-CC-I) (Hypertrachealosaeamic neuropeptide I).
OS	Periplaneta americana (American cockroach).
OS	Leptinotarsa decemlineata (Colorado potato beetle), and
OS	Blatta orientalis (Oriental cockroach).
OC	Bukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC	Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC	Blattidae; Periplaneta; Schistocerca; Blattaria; Blattoidea;
OC	NCBI_TaxID=6978, 7539, 6976;
RN	[1]
RP	SEQUENCE.
RC	SPECIES=P.americanus;
RX	Medline=84298179; PubMed=6551205;
RA	Scarborough R.M.; Jamieson G.C.; Kalish F.; Kramer S.J.; McEnroe G.A., Miller C.A.; Schooley D.A.;
RT	"Isolation and primary structure of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry."
RT	Biochem. Biophys. Res. Commun. 124:350-358 (1984).
RN	[2]
RP	SEQUENCE.
RC	SPECIES=P.americanus;
RX	Medline=84298179; PubMed=6551205;
RA	Rinehart K.L. JR.; Rinehart K.L. JR.;
RT	"Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry."
RT	Biochem. Biophys. Res. Commun. 124:350-358 (1984).
RN	[3]
RP	SEQUENCE.
RC	SPECIES=P.americanus;
RX	Medline=84298179; PubMed=6551205;
RA	Scarborough R.M.; Jamieson G.C.; Kalish F.; Kramer S.J.; McEnroe G.A., Miller C.A.; Schooley D.A.;
RT	"Isolation and primary structure of two peptides with cardioacceleratory and hyperglycemic activity from the corpora cardiaca of <i>Periplaneta americana</i> ."
RT	Biochem. Biophys. Res. Commun. 81:5575-5579 (1984).
RL	Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579 (1984).
RN	[4]
RP	SEQUENCE.
RC	SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX	Medline=90353659; PubMed=340112;
RA	Gaede G., Rinehart K.L. JR.;
RT	"Primary structures of hypertrachealosaeamic neuropeptides isolated from the corpora cardiaca of the cockroaches <i>Leucophaea maderae</i> , <i>Gromphadorhina portentosa</i> , <i>Blattella germanica</i> and <i>Blatta orientalis</i> and of the stick insect <i>Extatosoma tiaratum</i> assigned by tandem fast atom bombardment mass spectrometry";
RT	Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
CC	-1- FUNCTION: Hypertrachealosaeamic factors are neuropeptides that elevate the level of trehalose in the hemolymph (tritrophic is the major carbohydrate in the hemolymph of insects).
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- SIMILARITY: Belongs to the AKH / RPCH / HRTH / RPCH family.
CC	-1- SIMILARITY: Belongs to the AKH / RPCH family.
DR	PIR; A05169; A05169.
DR	PIR; A44960; A44960.
DR	PIR; A49823; A49823.
DR	PIR; S08995; S08995.
DR	InterPro; IPR002047; AKH.
DR	Prosite; PS00256; AKH; 1.
KW	Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	MOD_RES 8 8 AMIDATION.
SQ	SEQUENCE 8 AA; 991 MW; 86457789C452D6 CRC64;
Qy	Query Match 32 Local Similarity 75.0% Score 13; DB 1; Length 8; Best Local Similarity 75.0% Pred. No. 1.4e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	4 QYAF 7 1 QYNF 4
RESULT 8	FIBB_ERYPA STANDARD; PRT;
ID	FIBB_ERYPA
AC	P19346; Rel. 16, Created)
DT	01-NOV-1990 (Rel. 16, Last sequence update)
DT	01-NOV-1990 (Rel. 16, Last annotation update)
DE	Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN	FGB.
OS	Brythrocebus patas (Red quenon) (Hussar).
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC	Cercopithecinae; Erythrocebus.
OX	NCBI_TaxID=9538;
RN	[1]
RP	SEQUENCE.
RX	Medline=85289140; PubMed=3928610;
RA	Nakamura S., Takenaka O., Takahashi K.;
RT	"Fibrinopeptides A and B of Japanese monkey (<i>Macaca fuscata</i>) and patas monkey (<i>Brythrocebus patas</i>): their amino acid sequences, restricted mutations, and a molecular phylogeny for macaques, quenons, and baboons."
RT	J. Biochem. 97:1487-1492 (1985).
CC	-1- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.
CC	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC	-1- PM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains,

CC and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.

DR PIR: D24180; D24180.

DR InterPro: IPR002181; Fibronogen C.

DR PROSITE: PS00514; FIBRIN AG_C DOMAIN; PARTIAL.

KW Blood coagulation; Plasma.

FT PEPTIDE 1 9 FIBRINOPEPTIDE B.

NON TBR 9 9

SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 32.5%; Score 13; DB 1; Length 9;

Best Local Similarity 40.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DQVAF 7

DB 2 BEVLF 6

RESULT 9

AKH TABAT STANDARD; PRT; 8 AA.

AC P14595;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adiopokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)

DE (DCC 1).

OS Tabanus atratus (Horse fly)

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;

OC Tabanus.

NCBI_TaxID=7207;

RN [1]

RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RX MEDLINE=90046758; PubMed=2813385;

RA Jaffe H., Raina A. K., Riley C.T., Fraser B.A., Nachman R.J.,

RA Vogel V.W., Zhang Y.-S., Hayes D.K.;

RA primary structure of two neuropeptide hormones with adipokinetic and

RT hypotrehalosemic activity isolated from the corpora cardiaca of horse

RT flies (Diptera).;

RT Proc. Natl. Acad. sci. U.S.A. 86:8161-8164 (1989).

CC -i- FUNCTION: This hormone, released from cells in the corpora

CC cardiaca after the beginning of flight, causes release of

CC diglycerides from the fat body and then stimulates the flight

CC muscles to use these diglycerides as an energy source.

CC -i- SUBCELLULAR LOCATION: Secreted.

CC PIR: A33995; A33995.

DR InterPro: IPR002047, AKH.

DR PROSITE: PS00256; AKH_1.

KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.

FT MOD-RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD-RES 8 8 AMIDATION.

SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 30.0%; Score 12; DB 1; Length 8;

Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QYAF 7

Db 1 QYTFP 4

RESULT 10

AL18_CARMA STANDARD; PRT; 8 AA.

AC P81871;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DR Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579 (1984).

RN [2]

RP SEQUENCE.

RC SPECIES=P. americana;

RX MEDLINE=85046510; PubMed=6548628;

RA Witten J.L., Schaffner M.H., O'Shea M., Cook J.C., Hemling M.E.,

RA Rinella K.L. Jr.; Schooley D.A.;

RA Miller C.A.,

RA "Isolation and primary structure of two peptides with

RT cardioacceleratory and hyperglycemic activity from the corpora

RT cardaca of Periplaneta americana.";

RT Biochem. Biophys. Res. Commun. 124:350-358 (1984).

RN [3]

RP SEQUENCE.

RC SPECIES=L. decemlineata; TISSUE=Corpora cardiaca;

RX MEDLINE=90160053; PubMed=2576128;

RA Gaede G., Kellner R.;

RT "The metabolic neuropeptides of the corpus cardiacum from the potato

RT beetle and the American cockroach are identical.";

RT Peptides 10:1287-1289 (1989).

[4]

RN SEQUENCE; TISSUE=B; orientalis; corpora cardicae;
RC SPECIES=B; corpora cardicae;
RX MEDLINE=90253659; PubMed=2340112;

GAede G., Rinehart K.L. Jr.;
"primary structures of hypertrehalosaeic neuropeptides isolated from the corpora cardicae of the cockroaches *Leucophaea maderae*, and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombardment mass spectrometry.";
RT Grromphadorhina portentosa, Blattella germanica and Blatta orientalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry.";

RT Leucophaea maderae;

RT atom bombardment mass spectrometry.";

RT major carbohydrate in the hemolymph (trehalose is the major carbohydrate in the hemolymph of insects).

CC !- FUNCTION: Hypertrehalosaeic factors are neuropeptides that elevate the level of trehalose in the hemolymph (trehalose is the major carbohydrate in the hemolymph of insects).

CC !- SIMILARITY: Belongs to the ARH / HRTH / RPCH family.

CC !- SUBCELLULAR LOCATION: Secreted.

DR PIR; B49560; B49560.

DR PIR; B49823; B49823.

DR PIR; S08996; S08996.

DR InterPro; IPR002027; AKH.

DR PROSITE; PS00256; AKH; 1.

DR PROSITE; PS00256; AKH; 1.

KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 8 8 AMIDATION.

SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 30.0%; Score 12; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVAF 7
Db 1 QTSF 4

RESULT 13

NPMB_BOVIN

ID NPMB_BOVIN STANDARD; PRT; 8 AA.

AC P15507;

DT 01-APR-1990 (Rel. 14, Created)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Morphine modulating neuropeptide B.

OS Bos taurus (Bovine).

OC Buka-ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

RN RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Brain;

RX MEDLINE=86067985; PubMed=3865193;

RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;

RT "Isolation, sequencing, synthesis, and pharmacological characterization of two brain neuropeptides that modulate the action of morphine.";

RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761 (1985).

CC !- FUNCTION: Modulates the action of morphine.

CC !- SUBCELLULAR LOCATION: Secreted.

RT DR PIR; B24749; B24749.

RT Neuropeptide; Amidation.

FT MOD RES 8 8 AMIDATION.

SEQUENCE 8 AA; 1082 MW; 87D416C77D9C729 CRC64;

Query Match 30.0%; Score 12; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05; Indels 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLDQ 4
Db 1 FLFQ 4

RESULT 14

MOSF_CLYJA

ID MOSF_CLYJA STANDARD; PRT; 9 AA.

AC P19855;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-FEB-1991 (Rel. 17, Last annotation update)

DE [Phe-6]-mosact.

OS Clypeaster japonicus (Sand dollar).

OC Buka-ryota; Metazoa; Echinoidea; Eleutherozoa; Echinozoa;

OC Clypeasteridae; Clypeaster.

NCBI_TaxID=7644;

RN RP SEQUENCE.

RC TISSUE=;

RX MEDLINE=87052651; PubMed=2877794;

RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Primary structure and synthesis of a blocked myotropic neuropeptide isolated from the cockroach, *Leucophaea maderae*.";

RL Comp. Biochem. Physiol. 85C:219-224 (1986).

CC !- FUNCTION: Mediates visceral muscle contractile activity (myotropic activity).

CC !- MISCELLANEOUS: An analog without the N-terminal PCA residue was synthesized and found to exhibit greater activity (144t) than the parent neuropeptide. The portion of the sequence of LPK most critical for the myotropic properties is limited to the pentapeptide fragment FPPRL.

CC !- SIMILARITY: Belongs to the Pyrokinin family.

CC PIR; A23967; A23967.

DR InterPro; IPR001484; Pyrokinin.

DR InterPro; IPR001484; Pyrokinin.

RA Suzuki N., Kurita M., Yoshino K.I., Kajiura H., Nomura K., Yameguchi M.;

RT "Purification and structure of mosact and its derivatives from the egg jelly of the sea urchin *Clypeaster japonicus*.";

RL Zool. Sci. 4:649-656(1987).
 CC -1- FUNCTION: Stimulates sperm respiration and motility.
 DR PIR; JN0027; JN0027;
 SQ SEQUENCE 9 AA; 924 MW; 93245729CDC5BABS CRC64;

Query Match 30.0%; Score 12; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AFYV 9
 | :
 Db 5 AFLI 8

RESULT 15

ACI1_ACHI_ACHI
 ID ACHI_ACHI
 AC P35504;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE Achatina-L.
 OS Achatina fulica (Giant African snail)
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Styliommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;

[1] RN SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN=Perussac; TISSUE=Heart atrium;
 RX MEDLINE=892273551; PubMed=2597281;
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Novales E.T., Sun X.P., Yongsirikul A., Kim K.H., Novales-Li P.,
 RA "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica Perussac containing a D-amino acid residue";
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica Perussac containing a D-amino acid residue";
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=Perussac; TISSUE=Heart atrium;
 RX MEDLINE=9126856; PubMed=1675568;
 RA Fujimoto K., Kubota T., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.,
 RA "Purification of achatin-I from the atria of the African giant snail, Achatina fulica, and its possible function";
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=13939265;
 RA Ishida T., In Y., Doi M., Ito M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.,
 RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-Phe-Ala-Asp-Orn), an endogenous neuropeptide containing a D-amino acid residue";
 RT "D-amino acid residue";
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 -1- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency and produces a spike broadening of the identified heart excitatory neuron (PON); also enhances the amplitude and frequency of the heart beat. Has also an effect on several other muscles.
 DR PIR; A32480; A32480.
 KW Hormone; D-amino acid.
 MOD RES 2
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C8100000000 CRC64;
 Query Match 27.5%; Score 11; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLD 3
 Db 2 FAD 4

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OM protein - protein search, using sw model

Run on: February 24, 2004, 22:50:30 ; Search time 38 Seconds

(without alignments)
 74.728 Million cell updates/sec

Title: US-09-920-480B-1

Perfect score: 40
 Sequence: 1 FLDQYAFXV 9

Scoring table: BL05062

Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Maximum Match 0%

Listing First 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1.8	45.0	8 2	O09258	009258	synochococc	
2	1.5	37.5	8 11	Q99m0	Q99m0	mus musculus	
3	1.4	35.0	7 2	Q8RMS9	Q8RMS9	enterobacte	
4	1.4	35.0	8 11	Q99NK9	Q99NK9	hydrochoeru	
5	1.4	35.0	9 8	Q9GD36	Q9GD36	juncus effu	
6	1.3	32.5	7 13	Q8JU20	Q8JU20	gallus gallu	
7	1.3	32.5	8 2	Q8RQ49	Q8RQ49	buchnera ap	
8	1.3	32.5	8 2	Q53790	Q53790	streptococc	
9	1.3	32.5	8 2	Q8RQ57	Q8RQ57	buchnera ap	
10	1.3	32.5	9 2	P87568	P87568	streptococc	
11	1.3	32.5	9 9	Q8B9Z1	Q8B9Z1	cyanophage	
12	1.3	32.5	9 12	Q84333	Q84333	simian virus	
13	1.2	30.0	8 2	P72279	P72279	rhodococcus	
14	1.2	30.0	8 2	Q8GMMS	Q8GMMS	actinobact	
15	1.2	30.0	8 11	Q99MH2	Q99MH2	mus musculus	
16	1.2	30.0	8 11	Q9QVK5	Q9QVK5	rattus sp.	

Q46179 clostridium
 P78484 homo sapien
 Q81PT5 zea mays (m
 Q9QWG2 mus musculus
 Q7Z1C0 caenorhabdi
 Q9866 spinacia oil
 Q973X0 planktothri
 Q9H4D3 homo sapien
 Q8w892 diadema sav
 Q8w894 diadema mex
 Q9w896 diadema mex
 Q9w895 diadema ant
 Q9w893 diadema pau
 Q9wfr5 diadema pau
 Q9rku3 borrelia bu
 Q9r7H9 haemophilus
 Q14715 homo sapien
 Q9bqt4 homo sapien
 Q9225 mus musculus
 Q9wft4 diadema ant
 Q9wfs4 diadema mex
 Q9r7H9 laurencia v
 Q9mmf4 diadema mex
 Q9mmf4 buteo ruini
 Q9t1M7 buteo buteo
 Q9mmg9 buteo buteo
 Q9w8w5 diadema set
 Q9xJN0 bacteriophag
 Q9axH8 mesembrant

ALIGNMENTS

RESULT 1	ID	AC	PRELIMINARY;	PRT;	8 AA.
	009258	009258;			
		DT	01-JUL-1997 (TREMBLrel. 04; Created)		
		DT	01-JUL-1997 (TREMBLrel. 04; Last sequence update)		
		DT	01-DEC-2001 (TREMBLrel. 19; Last annotation update)		
		DE	NIFH		
		GN	Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).		
		OS	Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.		
		OC	NCBI - TaxID-41411;		
		RN	[1] -		
		RP	SEQUENCE FROM N.A.		
		RC	SEQUENCE=RP-1;		
		RX	MEDLINE=93231861; PubMed=10217509;		
		RA	Huang T.C.; Lin R.F.; Chu M.K.; Chen H.M.;		
		RT	"Organization and expression of nitrogen-fixation genes in the aerobic		
		RT	nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain		
		RT	Microbiology 145:743-753 (1999).		
		RL	DR EMBL: AF001780; AAC33369; 1. - .		
		FT	NON_TER 8 8		
		FT	SEQUENCE 8 AA; 985 MN; F16B59CD046C406 CRC64;		
		FT			
		Qy	4 QVAF 7 : : 3 QIAP 6		
		Db			

Q46179 clostridium
 P78484 homo sapien
 Q81PT5 zea mays (m
 Q9QWG2 mus musculus
 Q7Z1C0 caenorhabdi
 Q9866 spinacia oil
 Q973X0 planktothri
 Q9H4D3 homo sapien
 Q8w892 diadema sav
 Q8w894 diadema mex
 Q9w896 diadema mex
 Q9w895 diadema ant
 Q9w893 diadema pau
 Q9wfr5 diadema pau
 Q9rku3 borrelia bu
 Q9r7H9 haemophilus
 Q14715 homo sapien
 Q9bqt4 homo sapien
 Q9225 mus musculus
 Q9wft4 diadema ant
 Q9wfs4 diadema mex
 Q9r7H9 laurencia v
 Q9mmf4 diadema mex
 Q9mmf4 buteo ruini
 Q9t1M7 buteo buteo
 Q9mmg9 buteo buteo
 Q9w8w5 diadema set
 Q9xJN0 bacteriophag
 Q9axH8 mesembrant

RESULT 2	Q99m0	PRELIMINARY;	PRT;	8 AA.
	ID	Q99m0;		
	AC	Q99m0;		
	DT	01-JUN-2001 (TREMBLrel. 17; Created)		

DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)	DE	Amyloid beta protein (Fragment).
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	GN	APP.
DS	Adenosine deaminase tRNA-specific 1 (Fragment).		OS	Hydrochoerus hydrochaeris (Capybara) (Carpincho).
GN	ADAT1.		OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OS	Mus musculus (Mouse).		OC	Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;		OC	Hydrochoerus; Hydrochaeridae;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		OC	
OX	NCBI_TaxID=10090;		OX	
RN	[1]		RN	RN
RP	SEQUENCE FROM N.A.		RP	SEQUENCE FROM N.A.
RC	STRAIN=19/SvCj;		RC	MEDLINE=2108382; PubMed=11214319;
RX	MEDLINE=21231131; PubMed=11311948;		RX	Murphy W.J.; Ezizrik B.; Johnson W.E.; Zhang Y.P.; Ryder O.A.;
RA	Maas S.; Kim Y.G.; Rich A.;		RA	O'Brien S.J.;
RT	"Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two tRNA synthetases";		RT	"Molecular phylogenetics and the origins of placental mammals.";
RT	Mamm. Genome 12:387-393 (2001).		RL	Nature 409:514-618 (2001).
RL	EMBL; AF28904; AAC19310.1; -.		DR	EMBL; AA011342; AAG47377.1; -.
DR	MGD; MGI:1353531; Adat1.		FT	NON-TER 1 1
FT	NON-TER 8 8		FT	NON-TER 1 1
SQ	SEQUENCE 8 AA; 936 MW; F4D05B1AADC1B376 CRC64;		SQ	1356D686DB19C9C3 CRC64;
Qy	Query Match 37.5%; Score 15; DB 11; Length 8;		Query Match 35.0%; Score 14; DB 11; Length 8;	
	Best Local Similarity 50.0%; Pred. No. 1e+06;		Best Local Similarity 40.0%; Pred. No. 1e+06;	
	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
Db	3 DQVA 6 : : 5 DEIA 8		Db	2 FFFQOM 6 : : 2 FFFQOM 6
		RESULT 5		
		Q9SD36		SEQUENCE FROM N.A.
		ID Q9SD36		SEQUENCE FROM N.A.
		AC Q9SD36		PRELIMINARY;
		DT 01-MAR-2001		PRT;
		(TREMBLrel. 16, Created)		
		DT 01-MAR-2001		
		(TREMBLrel. 16, Last sequence update)		
		DT 01-JUN-2003		
		(TREMBLrel. 24, Last annotation update)		
		DE Ribosomal protein S16 (Fragment).		
		GN RPS16.		
		OS Juncus effusus (Soft rush).		
		OG Chloroplast.		
		OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
		OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Juncaceae; Juncus.		
		NCBI_TaxID=13579;		
		[1]		
		RN RP		
		SEQUENCE FROM N.A.		
		RC TISSUE-Leaf.		
		RA Asmussen C.B.; Chase M.W.;		
		RT Coding and noncoding plastid DNA in palm systematics ";		
		RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.		
		RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.		
		DR AJ40962; CAC17904.1; -.		
		DR GO; GO:0009507; C:chloroplast; IEA.		
		KW Chloroplast.		
		FT NON-TER 1 1		
		FT NON-TER 9 9		
		SQ SEQUENCE 9 AA; 1135 MW; 8DCCC9D2C046CB41 CRC64;		
		Query Match 35.0%; Score 14; DB 8; Length 9;		
		Best Local Similarity 50.0%; Pred. No. 1e+06;		
		Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
Qy	3 DQV 5 : : 2 DQI 4		Qy 4 QVAF 7 : : 4 QIVF 7	
		RESULT 6		
		Q8JJ20		SEQUENCE FROM N.A.
		ID Q8JJ20		SEQUENCE FROM N.A.
		AC Q8JJ20		PRELIMINARY;
		DT 01-OCT-2002		PRT;
		(TREMBLrel. 22, Created)		
		DT 01-OCT-2002		
		(TREMBLrel. 22, Last sequence update)		
		DE Extracellular fatty acid binding protein (Fragment).		
		GN EXFABP.		
		OS Gallus gallus (Chicken).		

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR	EMBL; M35285; AAA26912.1;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	DR	PTC; A7618; A47618;
OC	Gallus.	FT	NON-TER
OX		SQ	SEQUENCE 8
[1]	NCBI_TaxID=9031;		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BLOOD;		
RA	Wang Q.; Li N.; Li H.;	Query Match	32.5%; Score 13; DB 2; Length 8;
RT	"Cloning and sequencing of 3' UTR of EXFABP gene in chicken.";	Best Local Similarity	75.0%; Score 13; DB 2; Length 8;
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ/GenBank databases.	Matches	0; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;
DR	EMBL; AP487519; AAI96665.1;	QY	3 DQVA 6
FT	-	Db	4 DTVA 7
SQ	SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BEBB70 CRC64;		
		RESULT 9	
		Q9RQ57	PRELIMINARY;
		ID	Q9RQ57
		AC	Q9RQ57;
		DT	01-MAY-2000 (TREMBLrel. 13; Created)
		DT	01-MAY-2000 (TREMBLrel. 13; Last sequence update)
		DT	01-JUN-2001 (TREMBLrel. 17; Last annotation update)
		DE	NIFFS protein homolog (Fragment).
		GN	NIFTS
		OS	Buchnera aphidicola.
		OC	Bacterium; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
		OC	Enterobacteriaceae; Buchnera.
		NCBI_TaxID=9;	
		OX	
		RN	SEQUENCE FROM N.A.
		RP	MEDLINE=20022990; PubMed=10555290;
		RX	Clark M.A., Moran N.A., Baumann P.;
		RA	"Sequence evolution in bacterial endosymbionts having extreme base
		RA	compositions.";
		RT	RL. Mol. Biol. Evol. 16:1586-1598 (1999).
		RL	DR EMBL; AAI130812; AAF13797.1; -.
		FT	FT NON-TER 8
		SQ	SEQUENCE 8 AA; 980 MW; F3A7B504771A336 CRC64;
		Query Match	32.5%; Score 13; DB 2; Length 8;
		Best Local Similarity	66.7%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;
		Matches	
		QY	1 FLD 3
		Db	6 YLD 8
		RESULT 10	
		P82568	PRELIMINARY;
		ID	P82568
		AC	P82568;
		DT	01-OCT-2000 (TREMBLrel. 15; Created)
		DT	01-OCT-2000 (TREMBLrel. 15; Last sequence update)
		DT	01-OCT-2003 (TREMBLrel. 25; Last annotation update)
		DE	Unknown protein from 2D-page (Fragment).
		OS	Streptococcus pyogenes.
		OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
		OC	Streptococcus.
		NCBI_TaxID=1314;	
		OX	
		RN	SEQUENCE, AND MASS SPECTROMETRY.
		RP	STRAIN=JRS4;
		RC	RA Hogan D.A., Du P., Stevenson T.I., Whitten M., Kilby G.W., Rogers J., vanBogelen R.A.;
		RA	"Two-dimensional gel electrophoresis map of Streptococcus pyogenes proteins".
		RT	RL Submitted (MAY-2000) to Swiss-Prot; CC -1- MASS SPECTROMETRY; MW=22592.04; METHOD=ELECTROSPRAY.
		CC	FT NON-TER 1
		FT	SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;
		Query Match	32.5%; Score 13; DB 2; Length 9;
		RN	
		RP	SEQUENCE FROM N.A.
		RA	GILBERT H.J., Hall J.;
		RT	"Molecular cloning of streptococcus bovis lactose catabolic genes.";
		RL	J. Gen. Microbiol. 133:2285-2293 (1987).

Best Local Similarity 50.0%; Pred. No. 1e+06; Mismatches 2; Conservative 2; Last annotation update	Indels 0; Gaps 0; PRT; 8 AA.	PRIMINARY; PRT; 8 AA.
Qy 2 LDQV 5 Db 3 VDEV 6		
RESULT 11		
Q8H9Z1; PRELIMINARY; PRT; 9 AA.		
ID Q8H9Z1; AC Q8H9Z1; DT 01-MAR-2003 (TREMBLref. 23, Created) DT 01-MAR-2003 (TREMBLref. 23, Last sequence update) DT 01-MAR-2003 (TREMBLref. 23, Last annotation update) DE Capsid protein. OS Cyanophage S-KM1. OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae. OX NCBI_TaxID=187678; RN [1] _ RP SEQUENCE FROM N.A. RC STRAIN=S-KM1; RA Okunishi S.; Maeda H.; RT "Cyanophage in Kagoshima Bay"; RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases. DR AB080247; BAC54112.1; SQ SEQUENCE 9 AA; 1167 MW; DB9205AB59DB42D6 CRC64;		
Query Match Score 13; DB 9; Length 9; Best Local Similarity 50.0%; Pred. No. 1e+06; Mismatches 0; Conservative 3; Last annotation update	Indels 0; Gaps 0; PRT; 8 AA.	PRIMINARY; PRT; 8 AA.
Qy 4 QVAF 7 Db 2 QVYF 5		
RESULT 12		
Q8A333; PRELIMINARY; PRT; 9 AA.		
ID Q8A333; AC Q8A333; DT 01-NOV-1996 (TREMBLref. 01, Created) DT 01-NOV-1996 (TREMBLref. 01, Last sequence update) DT 01-DEC-2001 (TREMBLref. 19, Last annotation update) DE (Defective variant in 1449) with monkey alu-type insert DE (Fragment). OS Simian virus 40 (SV40). OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus. OX NCBI_TaxID=10633; RN		
RP SEQUENCE FROM N.A. MEDLINE=81054804; PubMed=6254029; RA Dhruva B.R.; Shenk T.; Subramanian K.N.; RT "Integration in vivo into Simian virus 40 DNA of a sequence that resembles a certain family of genomic interspersed repeated sequences"; RT Proc. Natl. Acad. Sci. U.S.A. 77:4514-4518 (1980). DR EMBL; K01001; AAA47875.1; -. FT NON_TER 9 9 MW; 802204044732C33A CRC64;		
Query Match Score 13; DB 12; Length 9; Best Local Similarity 50.0%; Pred. No. 1e+06; Mismatches 2; Conservative 2; Last annotation update	Indels 0; Gaps 0; PRT; 8 AA.	PRIMINARY; PRT; 8 AA.
Qy 2 LDQV 5 Db 1 MDKV 4		
RESULT 13		
Q8A335; PRELIMINARY; PRT; 8 AA.		
ID Q8A335; AC Q8A335; DT 01-MAR-2003 (TREMBLref. 23, Created) DT 01-MAR-2003 (TREMBLref. 23, Last sequence update) DT 01-JUN-2003 (TREMBLref. 24, Last annotation update) DE BPFB. Biphenyl dioxygenase (Fragment). GN BPFB. OS Rhodococcus globerulus. OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales. OC Corynebacteriaceae; Nocardiaceae; Rhodococcus. OX NCBI_TaxID=3308;		
RP SEQUENCE FROM N.A. MEDLINE=95255652; PubMed=7737502; RA Asturias J.A.; Diaz E.; Timmis K.N.; RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-positive bacterium Rhodococcus globerulus P6 to multicompartment dioxygenases of gram-negative bacteria."; RL Gene 156:11-18 (1995). EMBL; X80041; CAU56350.1; -. DR GO:0016702; F:oxidoreductase activity, acting on single d...; IEA. KW DR GO:0016702; F:oxidoreductase activity, acting on single d...; IEA. FT NON_TER 8 MW; 8 EBD2C81AB6D73406 CRC64;		
Query Match Score 12; DB 2; Length 8; Best Local Similarity 66.7%; Pred. No. 1e+06; Mismatches 0; Conservative 2; Last annotation update	Indels 0; Gaps 0; PRT; 8 AA.	PRIMINARY; PRT; 8 AA.
Qy 3 DQV 5 Db 5 DEV 7		
RESULT 14		
Q8GMM5; PRELIMINARY; PRT; 8 AA.		
ID Q8GMM5; AC Q8GMM5; DT 01-MAR-2003 (TREMBLref. 23, Created) DT 01-MAR-2003 (TREMBLref. 23, Last sequence update) DE TNP17. GN TNP17. OS Acinetobacter sp. BW3. OG Plasmid; PKLH207. OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales. OC Moraxellaceae; Acinetobacter. OX NCBI_TaxID=106335; RN		
RP SEQUENCE FROM N.A. RC STRAIN=BW3; PLASMID=PKLH207; RA Kholidii G.Y.; Yurieva O.V.; Gorlenko Z.M., Gorlenko Z.M., RA Nikiforov V.G.; RA Petrova M.A.; Nikiforov V.G.; RA "PKLH2-like aberrant transposons and possible mechanisms of their dissemination"; RT RT the Acinetobacter genus"; RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases. DR EMBL; AJ250234; CAC8784.1; -. DR GO:0046821; CAC8784.1; -. DR GO:0046821; C:extrachromosomal DNA; IEA. KW Plasmid.		
Query Match Score 12; DB 2; Length 8; Best Local Similarity 75.0%; Pred. No. 1e+06;	Indels 0; Gaps 0; PRT; 8 AA.	PRIMINARY; PRT; 8 AA.
Qy 2 LDQV 5 Db 1 MDKV 4		

	Matches	3 ;	Conservative	0 ;	Mismatches	1 ;	Indels	0 ;	Gaps	0 ;
Qy	2	LdQV 5								
Db	3	LtQV 6								

RESULT 15

Q99MH2 PRELIMINARY; PRT; 8 AA.
 ID Q99MH2; AC 099MH2; DT 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBrel. 17, Last annotation update)
 DB Cyclooxygenase 2 (Fragment).
 OS Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RN
 RP
 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Claycombe K.J., Paulson E., Wu D., Meydani S.N.;
 PT "Mouse cyclooxygenase 2 (COX-2) gene expression regulation."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AF344876; AAC27680.1; -
 FT NON-TER 1
 FT NON-TER 8 8
 SQ SEQUENCE 8 AA; 911 MW; AC087DD046C411BA CRC64;
 Query Match 30.0%; Score 12; DB 11; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e-06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 QVA 6
 |:
 Db 4 QIA 6

Search completed: February 24, 2004, 22:56:52
 Job time : 42 secs

Run on:	February 24, 2004, 22:26:09 ; Search time 52 Seconds	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	RESULT 1 ID AAU09698 Standard; peptide; 9 AA. XX AAU09698; XX AC DT 26-MAR-2002 (first entry) XX DE Anti-melanoma compound #3. XX KW Human; anti-melanoma compound; melanoma antigen gp100; APC; MHC; mutant; immune effector cell; antigen presenting cell; anti-cancer; mutant; major histocompatibility complex; gp100 tumour antigen; cytostatic. XX KW Homo Sapiens. OS Synthetic. XX PN WO200192294-A2. XX XX PD 06-DEC-2001. XX PF 21-MAY-2001; 2001WO-US016417. XX PR 31-MAY-2000; 2000US-0208955P. PR 09-FEB-2001; 2001US-0267B77P. XX PA (GENZYME CORP. XX PI Nicolette CA; XX DR WPI; 2002-106301/14.
Scoring table:	BLOSUM62	Score: 40	Score: 40
Perfect score:	Gapop 10.0 , Gapext 0.5	Scoring table: BLOSUM62	Scoring table: BLOSUM62
Sequence:	1 FLDQYAFXV 9	Sequence: 1 FLDQYAFXV 9	Sequence: 1 FLDQYAFXV 9
Total number of hits satisfying chosen parameters:	281240	Total number of hits satisfying chosen parameters:	281240
Minimum DB seq length:	0	Minimum DB seq length:	0
Maximum DB seq length:	9	Maximum DB seq length:	9
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries		Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database :	A_Genseq_29Jan04:*	Database :	A_Genseq_29Jan04:*
1: genseqp1980s:*	1: genseqp1980s:*	1: genseqp1980s:*	1: genseqp1980s:*
2: genseqp2000s:*	2: genseqp2000s:*	2: genseqp2000s:*	2: genseqp2000s:*
3: genseqp2001s:*	3: genseqp2001s:*	3: genseqp2001s:*	3: genseqp2001s:*
4: genseqp2002s:*	4: genseqp2002s:*	4: genseqp2002s:*	4: genseqp2002s:*
5: genseqp2003s:*	5: genseqp2003s:*	5: genseqp2003s:*	5: genseqp2003s:*
6: genseqp2003s:*	6: genseqp2003s:*	6: genseqp2003s:*	6: genseqp2003s:*
7: genseqp2004s:*	7: genseqp2004s:*	7: genseqp2004s:*	7: genseqp2004s:*
8: genseqp2004s:*	8: genseqp2004s:*	8: genseqp2004s:*	8: genseqp2004s:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	*
		SUMMARIES	
Result No.	Score	Query Match Length DB ID	Description
1	39	97.5 9 5 AAU09698	AAU09698 Anti-mela
2	38	95.0 9 3 AAYB8764	AAYB8764 Anti-genic
3	38	95.0 9 3 AAYB8763	AAYB8763 Anti-genic
4	38	95.0 9 5 AAU09697	AAU09697 Anti-mela
5	34	85.0 9 2 AAR84835	AAR84835 Modified
6	34	85.0 9 3 AAY84766	AAY84766 Anti-genic
7	34	85.0 9 4 AAU28984	Aau28984 Modified
8	34	85.0 9 5 AAU09696	AAU09696 Anti-mela
9	34	85.0 9 7 ADB97751	ADB97751 Human gp1
10	31	77.5 9 2 AAR84836	Aar84836 Modified
11	31	77.5 9 4 AAU28985	Aau28985 Modified
12	31	77.5 9 7 ADB97752	ADB97752 Human gp1
13	29	72.5 9 2 AAR84834	Aar84834 Modified
14	29	72.5 9 2 AAR84819	Aar84819 Modified
15	29	72.5 9 3 AAYB8769	AAYB8769 Anti-genic
16	29	72.5 9 4 AAU28983	AAU28983 Modified
17	29	72.5 9 4 AAU28968	Aau28968 Modified
18	29	72.5 9 7 ADB97735	ADB97735 Human gp1
19	29	72.5 9 7 ADB97750	ADB97750 Human gp1
20	28	70.0 9 2 AAR84816	Aar84816 Modified
21	28	70.0 9 2 AAY55577	AAY55577 HLA bindi
22	28	70.0 9 2 AAY55434	AAY55434 HLA bindi
23	28	70.0 9 2 AAY55255	AAY55255 HLA bindi
24	28	70.0 9 4 AAU28965	Aau28965 Modified
25	28	70.0 9 4 AAB47533	Aab47533 Anti-mela

The present invention relates to anti-melanoma compounds comprising a peptide sequence based on human melanoma antigen gp100. Also described are antibodies that recognise and bind to these compounds, and immune effector cells, polynucleotides that encode these compounds, and immune effector cells that have been raised in vitro or in vivo in the presence of an antigen presenting cell (APC) that presents the compound. Such an APC may be the major histocompatibility complex (MHC) molecule. The anti-melanoma compounds are useful for inducing an immune response in a subject, by delivering the compound to the subject in the context of an MHC molecule which presents the compound on the surface of an APC. The anti-melanoma

compound is delivered as a polynucleotide that encodes it. The compounds are useful to generate antibodies that specifically recognise and bind to them, for the treatment of melanoma, as components of anti-cancer vaccines, and to expand immune effector cells that are specific for cancers characterised by expression of gp100 tumour antigen, melanoma. The compounds are also useful in diagnostic methods for such diseases. AAU0696-AAU09705 represent the anti-melanoma compounds of the invention encoded by degenerate DNA sequences as shown in AAS14397-AAS14406 respectively.

Sequence 9 AA:
 Query Match 97.5%; Score 39; DB 5; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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  1 FLDQVAXV 9
  | | | | |
  1 FLDQVAFSV 9
  | | | | |
  1 FLDQVAFSV 9
  
```

SULT 2
Y84764
AY84764 standard; peptide: 9 AA.
AY84764;

08-AUG-2000 (First entry)
Antigenic peptide epitope of α 1100 polypeptide

Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R; tumour antigen; vaccine; tumour cell; immune response; gp100.

Synthetic.

WO200020457-A1

卷之三

INTERZASSA - OMEEC 1997 100 10

9805-001-1998; 9805-0103229P.

11-FEB-1999; 99US-0120001P.

THE JOURNAL OF CLIMATE

(GENZ) GENZIME CORP.

Nicolette CA;

WPI: 2000-303749/26.

Now: *symbolic* *antinomies* 17

factor receptor, useful as vaccine

Claim 11: Page 92: 116nm: English

AAV84763-69 represent synthetic antigenic peptide epitopes of gp100. The specification also describes synthetic epitopes of insulin-like Growth factor II receptor (IGF-II-R). The synthetic peptides bind to a MHC class I or class II molecule with a higher affinity than the natural sequence. The synthetic antigenic peptide epitopes may correspond to tumour antigens, and are therefore useful as vaccines against tumour cells expressing cell surface tumour antigen. They are also useful in a variety of methods of modulating an immune response to the synthetic antigenic peptide epitopes and thus to the corresponding native antigenic determinant. The synthetic antigenic peptide epitopes find application in a wide variety of immunomodulatory protocols, including methods to induce or increase an immune response, as well as in methods to suppress or reduce an undesirable immune response to a corresponding natural epitope

determinant. The synthetic antigenic peptide epitopes find application in a wide variety of immunodiagnostic protocols, including methods to induce or increase an immune response, as well as in methods to suppress or reduce an undesirable immune response to a corresponding natural antigen.

Query Match 77.5%; Score 31; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLDQVAFXY 9
 :||| | |
 Db 1 YLDQVPPSV 9

RESULT 11
 AAU23985
 ID AAU23985 standard; peptide; 9 AA.
 AC AAU23985;
 XX DT 18-DEC-2001 (first entry)
 DE Modified gp100 G9-209 peptide #21.
 XX Human; MART-1; immunogenic; melanoma antigen recognised by T lymphocyte;
 KW diagnostic; therapeutic; vaccine; melanoma; in vivo tumour recognition;
 KW in vivo tumour rejection.
 XX Synthetic.
 OS
 XX PN US6270778-B1.
 XX PD 07-AUG-2001.
 XX PF 12-MAR-1999; 99US-00267439.
 XX PR 22-APR-1994; 94US-00231565.
 PR 05-APR-1995; 95US-00417174.
 PR 05-MAY-1988; 98US-00073138.
 (USSR) US DEPT HEALTH & HUMAN SERVICES.
 XX Kawakami Y, Rosenberg SA,
 PI WPI; 2001-595403/67.
 XX Immunogenic peptide useful in vaccines comprises specific amino acids of
 PT new melanoma antigen recognized by T lymphocytes.
 PT Example 5; Col 55; 73pp; English.
 XX The invention relates to a novel immunogenic peptide comprising 5-20
 CC contiguous amino acids of new melanoma antigen recognised by T
 CC lymphocytes (MART-1). The peptide sequence contains at least one amino
 CC acid modification of MART-1. The peptide is used in diagnostic and
 CC therapeutic methods as an immunogen or vaccine to prevent or treat
 CC melanoma, and for in vivo tumour recognition and rejection. AAU28898-
 CC 0008 represent MART-1 peptide amino acid sequences, and related
 CC sequences of the invention.
 XX Sequence 9 AA;
 XX Query Match 77.5%; Score 31; DB 4; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLDQVAFXY 9
 :||| | |
 Db 1 YLDQVPPSV 9

RESULT 12
 ADB7752
 ID ADB7752 standard; peptide; 9 AA.
 XX AC ADB97752;
 XX

DT 04-DEC-2003 (first entry)
 XX Human gp100 antigenic peptide #12 analogue #21.
 DE
 KW Human; melanoma antigen recognised by T-lymphocytes; MART-1; melanoma;
 KW skin cancer; T lymphocyte; cytosatic; gene therapy; vaccine; antigen;
 KW major histocompatibility complex; MHC; human leukocyte antigen; HLA-A2;
 KW tumour infiltrating lymphocyte; mutant; muttein.
 XX Synthetic.
 OS
 OS Homo sapiens.
 XX PN US2003144482-A1.
 XX PD 31-JUL-2003.
 XX PF 03-JUL-2001; 2001US-00898860.
 XX PR 22-APR-1994; 94US-00231565.
 PR 12-MAR-1999; 99US-00267439.
 XX PA (KAWA/) KAWAKAMI Y.
 (ROSE/) ROSENBERG S A.
 XX PI Kawakami Y, Rosenberg SA;
 XX DR WPI; 2003-755536/1.
 XX PT New immunogenic peptides derived from melanoma antigens recognized by T-
 lymphocytes or from gp100, useful for preventing or treating melanoma.
 XX PR Example 5; Page 31; 77pp; English.
 PS
 XX The invention relates to an immunogenic peptide having contiguous amino
 acids derived from the sequence of melanoma antigens recognised by T-
 CC lymphocytes (MART-1) or gp100. The MART-1 sequence appears as ADB97651,
 CC and the gp100 (differing by 1 amino acid from the previously published
 CC gp100 (ADB97770) appears as ADB97676. Also included are a pharmaceutical
 CC composition (comprising the above peptide and an excipient, diluent or
 CC carrier), a vaccine for immunising a mammal (comprising the above peptide
 CC in a carrier), preventing or treating melanoma (comprising administering
 CC the above composition to a mammal in an amount to stimulate the
 CC production of protective antibodies or immune cells), a purified and
 CC isolated nucleic acid sequence encoding the above peptide, a recombinant
 CC expression vector comprising at least one nucleic acid sequence cited
 CC above, a host organism transformed or transfected with the vector
 CC (expressing the peptide) and antibodies reactive with the above
 CC immunogenic peptide. The peptide sequence contains at least one amino
 CC acid modification (amino acid substitution) of the MART-1 or gp100
 CC sequence to enhance binding of the peptide to a Major Histocompatibility
 CC Complex (MHC) molecule. The peptide is recognised by Human Leukocyte
 CC Antigen (HLA)-A2 restricted tumour infiltrating lymphocytes. The peptide
 CC composition and methods are useful in preventing or treating melanoma and
 CC skin cancer. The present sequence represents a modified melanoma
 CC antigenic peptide of the invention.
 XX Sequence 9 AA;
 XX Query Match 77.5%; Score 31; DB 7; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLDQVAFXY 9
 :||| | |
 Db 1 YLDQVPPSV 9

RESULT 13
 AAR84834
 ID AAR84834 standard; peptide; 9 AA.
 XX AC AAR84834;
 XX

DT	25-APR-1996	(First entry)
DE	Modified melanocyte-melanoma specific antigenic peptide G9-209-1W2L.	
XX		
KW	MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;	
KW	metastatic melanoma; tumour-associated antigen; immunogenic peptide;	
KW	diagnosis; prognosis; prophylaxis; therapy; vaccine.	
XX		
OS	Synthetic.	
XX		
PN	WO9529193-A2.	
XX		
PD	02-NOV-1995.	
XX		
PF	95WO-US005063.	
XX		
PR	21-APR-1995;	
XX		
PR	22-APR-1994;	94US-00231565.
XX		
PR	05-APR-1995;	95US-00417174.
XX		
PA	(USSH) US SEC DEPT HEALTH.	
XX		
PI	Kawakami Y, Rosenberg SA;	
XX		
DR	WPI: 1995-382963/49.	
XX		
PT	DNA encoding melanoma antigens recognised by T-lymphocytes - also	
PT	vectors host cells and antibodies, used to detect, treat and immunise	
PT	animal against melanoma.	
XX		
PS	Example 5: Page 107; 184DP; English.	
XX		
CC	AAR8416-836 are G9-209 peptides modified to improve immunogenicity. G9-209 is an immunogenic peptide based on the melanoma derived antigen, gp100 (see AAR84210). The peptides are used in medicaments for the treatment or prevention (by immunization) of melanoma. Antibodies against MART-1 and its immunogenic peptides may be used in the detection and isolation of MART-1 from a sample, the detection of which is indicative of a disease state (melanoma or metastatic melanoma)	
CC		
CC	Example 5: Page 107; 184DP; English.	
CC		
CC	Sequence 9 AA;	
XX		
CC	Query Match 72.5%; Score 29; DB 2; Length 9;	
CC	Best Local Similarity 66.7%; Pred. No. 1.4e+06;	
CC	Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
CC		
CC	1 FLDQYAFXV 9	
CC	1 WLDQYFVFSV 9	
XX		
Qy	RESULT 14	
XX	AAR84819	
ID	AAR84819 standard; peptide; 9 AA.	
XX		
AC	AAR84819;	
XX		
DT	25-APR-1996 (First entry)	
XX		
DE	Modified melanocyte-melanoma specific antigenic peptide G9-209-1F.	
XX		
KW	MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;	
KW	metastatic melanoma; tumour-associated antigen; immunogenic peptide;	
KW	diagnosis; prognosis; prophylaxis; therapy; vaccine.	
XX		
OS	Synthetic.	
XX		
PN	WO9529193-A2.	
XX		
PD	02-NOV-1995.	
XX		
PF	95WO-US005063.	
XX		
PR	22-APR-1994; 94US-00231565.	

PR 05-APR-1995; 95US-00417174.
 XX (USSH) US SEC DEPT HEALTH.
 XX
 PI Kawakami Y, Rosenberg SA;
 XX DR WPI; 1995-382963/49.
 XX PT DNA encoding melanoma antigens recognised by T-lymphocytes - also
 PT vectors, host cells and antibodies, used to detect, treat and immunise
 PT animal against melanoma.
 XX PS Example 5; Page 107; 184pp; English.
 XX AAR84816-836 are G9-209 peptides modified to improve immunogenicity. G9-
 CC 209 is an immunogenic peptide based on the melanoma derived antigen, G9-
 CC GP100 (see AAR84210). The peptides are used in medicaments for the
 CC treatment or prevention (by immunization) of melanoma. Antibodies against
 CC MART-1 and its immunogenic peptides may be used in the detection and
 CC isolation of MART-1 from a sample, the detection of which is indicative
 CC of a disease state (melanoma or metastatic melanoma)
 XX SQ Sequence 9 AA;
 XX Query Match 72.5%; Score 29; DB 2; Length 9;
 CC Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 CC Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 CC
 QY 1 FLDQVAFXV 9
 DB 1 FTDQVAFPSV 9
 XX
 RESULT 15
 AAY84769
 ID AAY84769 standard; peptide; 9 AA.
 XX
 AC AAY84769;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Antigenic peptide epitope of gp100 polypeptide.
 XX
 KW Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;
 XX tumour antigen; vaccine; tumour cell; immune response; gp100.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5
 FT /note= "any amino acid"
 FT Misc-difference 6
 FT /note= "any amino acid"
 FT Misc-difference 8
 FT /note= "any amino acid"
 XX WO200020457-A1.
 PN
 XX 13-APR-2000.
 PD
 XX 04-OCT-1999; 99WO-US023167.
 XX
 PR 05-OCT-1998; 98US-0103229P.
 PR 05-JAN-1999; 99US-0114811P.
 PR 11-FEB-1999; 99US-0120001P.
 XX
 PA (GENZ) GENZYME CORP.
 XX
 PI Nicolette CA;
 XX
 DR WPI; 2000-30374/26.

New synthetic antigenic peptide epitopes related to insulin-like growth factor receptor, useful as vaccines against tumor cells expressing cell surface tumor antigen.

Claim 17: Page 92: 116pp: English

AAV84763-69 represent synthetic antigenic peptide epitopes of gp100. The specification also describes synthetic epitopes of insulin-like growth factor II receptor (IGF-II-R). The synthetic peptides bind to a MHC class I or class II molecule with a higher affinity than the natural sequence. The synthetic antigenic peptide epitopes may correspond to tumour antigens, and are therefore useful as vaccines against tumour cells expressing cell surface tumour antigen. They are also useful in a variety of methods of modulating an immune response to the synthetic antigenic peptide epitopes and thus to the corresponding native antigenic determinant. The synthetic antigenic peptide epitopes find application in a wide variety of immunomodulatory protocols, including methods to induce or increase an immune response, as well as in methods to suppress or reduce an undesirable immune response to a corresponding natural epitope

Sequence 9 AA:

```

Query Match      72.5%;  Score 29;  DB 3;  Length 9;
Best Local Similarity 77.8%;  pred. No. 1.4e+06;
Matches 7;  Conservative 0;  Mismatches 2;  Indels 0;  Caps 0;
Qy      1 FLDQYAFXV 9
Db      1 FLDQXXFXV 9

```

Search completed: February 24, 2004, 22:55:35
Search time : 54 seconds

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:33:10 ; Search time 21 Seconds
(without alignments)
41.225 Million cell updates/sec

Title: US-09-920-480B-3
Perfect score: 47

Sequence: 1 FLFSWYAXV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*

1: Piri:*

2: Piri:*

3: Piri:*

4: Piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	55.3	9	2 I46023	Growth hormone receptor - bovine (fragment)
2	20	42.6	9	2 S56004	C;Species: Bos primigenius taurinus (cattle)
3	18	38.3	7	2 PN0230	C;Accession: I46023
4	18	38.3	7	2 PN0649	R.Hauser, S.D.; McGrath, M.F.; Collier, R.J.; Krivi, G.G.
5	18	38.3	8	2 JS0318	Mol. Cell. Endocrinol 72, 187-200, 1990
6	18	38.3	8	2 T13819	A;Title: Cloning and <i>in vivo</i> expression of bovine growth hormone receptor mRNA.
7	18	38.3	9	2 A24244	A;Reference number: I46023; PMID:91146804;
8	16	34.0	8	2 S10596	A;Accession: I46023
9	16	34.0	8	2 P02479	A;Status: preliminary; translated from GB/EMBL/DDJB
10	15	31.9	4	2 PT0661	A;Residues: 1-9 <HAT>
11	15	31.9	5	2 PT0580	A;Cross-references: EMBL:U24113; NID:9775221; PIDN:AAA91014.1; PMID:9775223
12	15	31.9	6	2 A31263	C;Generics:
13	15	31.9	6	2 A61068	A;Gene: GHR
14	15	31.9	7	2 A61081	RESULTS
15	15	31.9	8	2 JS0315	1 FFLFSWYAXV 9
16	15	31.9	8	2 JS0316	Query Match 55.3%; Score 26; DB 2; Length 9;
17	15	31.9	8	2 JS0317	Best Local Similarity 44.4%; Pred. No. 2.8e+05;
18	15	31.9	9	2 A38887	Mismatches 1; Indels 0; Gaps 0;
19	15	31.9	9	2 D57444	RESULTS
20	15	31.9	9	2 PT0272	1 FQFPWFVIV 9
21	15	31.9	9	2 PT0299	Query Match 55.3%; Score 26; DB 2; Length 9;
22	15	31.9	9	2 PT0315	Best Local Similarity 40.0%; Pred. No. 2.8e+05;
23	15	31.9	9	2 I58350	Mismatches 2; Indels 0; Gaps 0;
24	14	29.8	7	1 NGP7	RESULTS
25	14	29.8	9	2 C24180	1 FQFPWFVIV 9
26	14	29.8	9	2 A43848	Query Match 42.6%; Score 20; DB 2; Length 9;
27	13	27.7	6	2 PD0048	Best Local Similarity 40.0%; Pred. No. 2.8e+05;
28	13	27.7	7	2 PX0008	Mismatches 2; Indels 0; Gaps 0;
29	13	27.7	8	2 A28804	RESULTS

ALIGNMENTS

30	13	27.7	8	2 S08996	hypertrehalosemic adipokinetic hormo
31	13	27.7	8	2 B49223	neuropeptide Led-C
32	13	27.7	8	2 B44380	glycine reductase
33	13	27.7	8	2 A39308	blood cell protein
34	13	27.7	8	2 S68325	52.5K protein - sp
35	13	27.7	9	2 S78226	IG heavy chain CRD
36	12	25.5	6	2 PT0231	alcohol dehydrogen
37	12	25.5	6	2 S66795	dihydrofolate redu
					T-cell receptor be
					venom heptapepti
					hypothetical prote
					H2 class I protein
					virotoxin - destro
					hypertrehalosemic
					adipokinetic hormo

RESULT 3

Db :||| 5 YSW 7

desmorphin (TRP-4, Asn-7) [validated] - two-colored leaf frog (fragment)

C;Species: *Phyllomedusa bicolor* (two-colored leaf frog)

C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000

C;Accession: S21230

R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Ersamer, G.; Kreil, G.

FEBS Lett. 302, 151-154, 1992.

A;Title: Identification and characterization of two dermorphins from skin extracts of the *Phyllomedusa bicolor* frog.

A;Reference number: S21152; MUID:92339502; PMID:1633846

A;Accession: S21230

A;Molecule type: protein

A;Residues: 1-7 <MIG>

C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 38.3%; Score 18; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WI 6

Db 4 WY 5

RESULT 4

PN0649

pullulanase (EC 3.2.1.41) - *Bacillus* sp. (strain S-1) (fragment)

C;Species: *Bacillus* sp.

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 03-Jun-2002

C;Accession: PN0649

R;Kim, C.H.; Choi, H.I.; Lee, D.S.

Biotech. Biotechnol. Biochem. 57, 1632-1637, 1993

A;Title: Purification and biochemical properties of an alkaline pullulanase from alkalo-

A;Reference number: PN0649; MUID:94080025; PMID:7764261

A;Molecule type: protein

A;Accession: PN0649

A;Residues: 1-7 <KIM>

C;Comment: This enzyme is used together with glucosamylase to improve the efficiency of starch in high maltose syrups.

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 38.3%; Score 18; DB 2; Length 7;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SWY 6

Db 5 SWF 7

RESULT 5

JS0318

leucokinin VIII - Madeira cockroach

C;Species: *Leucophaea maderae* (Madeira cockroach)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C;Accession: JS0318

R;Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 89, 31-34, 1987

A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the first leucokinins.

A;Reference number: JS0317

A;Molecule type: protein

A;Residues: 1-8 <ROL>

C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act-

C;Keywords: amidated carboxyl end; cephalomyotropic peptide

F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 38.3%; Score 18; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FSW 5

RESULT 6

T13818

Cytochrome oxidase subunit I - Atlantic halibut *Myoxine glutinosa* (Atlantic halibut)

C;Species: mitochondrial Myoxine glutinosa (Atlantic halibut)

C;Accession: T13818

R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.

Mol. Biol. Evol. 14, 807-813, 1997

A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI

A;Reference number: Z17775; MUID:97338704; PMID:9255918

A;Accession: T13818

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-8

A;Cross-references: EMBL:Y09527; NID:92340019; PIDN:CAA70718.1; PID:g2340022

C;Genetics:

A;Genome: COI

A;Note: COI

C;Keywords: mitochondrion

Query Match 38.3%; Score 18; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLESWY 6

Db 2 YLSRWF 7

RESULT 7

A24244

adipokinetic hormone - bollworm

N;Alternative names: Hez-AKH

C;Species: *Heliothis zea* (bollworm, corn earworm, tomato fruitworm)

C;Accession: A24244

R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway Biochem. Biophys. Res. Commun. 135, 622-628, 1986

A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helicoverpa armigera. A reference number: A24244; MUID:3964263

A;Accession: A24244

A;Molecule type: protein

A;Residues: 1-9 <JAF>

C;Superfamily: adipokinetic hormone

F;8/Modified site: pyrrolidone carboxylic acid (Gly) #status experimental

F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 38.3%; Score 18; DB 2; Length 9;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLESW 5

Db 4 FTSSW 8

RESULT 8

S10596

adipokinetic hormone - pond skimmer

C;Species: *Libellula auripennis*

C;Accession: S10596

R;Gaedt, G.

Biol. Chem. Hoppe-Seyler 371, 475-483, 1990

A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hc

A;Reference number: S10596; MUID:90359055; PMID:2330213

A;Molecule type: protein

A;Residues: 1-8 <BIO>
 C;Comment: This peptide has both adipokinetic and hypertrehalosemic activities.
 C;Species: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1;Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;2;Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 34.0%; Score 16; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLPSW 5
 Db 4 FTPSW 8

RESULT 9
 B2449
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
 C;Accession: B24749
 R;Yang, H.Y.T.; Fratella, W.; Majane, E.A.; Costa, E.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
 A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two bovine
 A;Reference number: A94074; PMID:86067985; PMID:3865193
 A;Accession: B24749
 A;Molecule type: protein
 A;Residues: 1-8 <AN>
 C;Superfamily: unassigned animal peptides
 C;Keywords: neuropeptide

Query Match 34.0%; Score 16; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLF 3
 Db 1 FLF 3

RESULT 10
 PT0661
 T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 R;Feeaney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0661
 A;Accession: PT0661
 R;Feeaney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0661
 A;Accession: PT0661
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 4 postnatal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 31.9%; Score 15; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SW 5
 Db 2 SW 3

RESULT 11
 PT0580
 T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0580

R;Feeaney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0580
 A;Accession: PT0580
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-5 <FEE>
 A;Experimental source: day 19 fetal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 31.9%; Score 15; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 SW 5
 Db 3 SW 4

RESULT 12
 A31263
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
 C;Species: Plasmodium falciparum
 C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
 C;Accession: A31263
 R;Peterson, D.S.; Walliker, D.; Wellens, T.E.
 Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
 A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
 A;Reference number: A94217; PMID:89057886; PMID:2904149
 A;Accession: A31263
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-6 <PT>
 C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 31.9%; Score 15; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SW 5
 Db 2 SW 3

RESULT 13
 A61068
 Locustakinin - migratory locust
 C;Species: Locusta migratoria (migratory locust)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
 C;Accession: A61068
 R;Schoots, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
 Regul. Pept. 37, 49-57, 1992
 A;Title: Locustakinin, a novel myotropin peptide from Locusta migratoria, isolation, pri
 A;Reference number: A61068; PMID:9226285; PMID:1585017
 A;Accession: A61068
 A;Molecule type: protein
 A;Residues: 1-6 <SCH>
 C;Keywords: amidated carboxyl end; cephalomyotropin peptide; neuropeptide
 F;6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 31.9%; Score 15; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SW 5
 Db 4 SW 5

RESULT 14
 A61081
 tryptophyllin, basic - Rohde's leaf frog

C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
 C;Accession: A61081
 R;Montecuccchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Ersamer, V.
 Int. J. Pest. Protein Res. 33, 391-395, 1989
 A;Title: Isolation, structure determination and synthesis of a novel tryptophan-containin
 A;Reference number: A61081
 A;Accession: A61081
 A;Molecule type: protein
 A;Residues: 1-7 <MON>
 C;Comment: The biological activity of this peptide was not determined.
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end; hydroxyproline; skin
 F;7/Modified site: 4-hydroxyproline (Pro) #status experimental
 F;7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match Score 15; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 SW 5
 Db 4 SW 5

RESULT 15
 JS0315
 Leucokinin V - Madeira cockroach
 C;Species: Leucophaea madraea (Madeira cockroach)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C;Accession: JS0315
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 27-30, 1987
 A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic
 A;Reference number: JS0315
 A;Accession: JS0315
 A;Molecule type: protein
 A;Residues: 1-8 <HOU>
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match Score 15; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 SW 5
 Db 6 SW 7

Search completed: March 18, 2004, 13:36:55
 Job time : 22 secs

GenCore version 5.1.6
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OM Protein - protein search, using sw model

Run on: March 18, 2004, 13:29:30 ; Search time 11 Seconds

Title: US-09-920-480B-3
 Perfect score: 47
 Sequence: 1 FLFSWYAXV 9

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Maximum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Prob. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	18	38.3	8	1	LCK8 LEUNA	P1990	P1990; DT 01-FEB-1991 (Rel. 17, Created) DT 01-FEB-1991 (Rel. 17, Last sequence update)
2	16	34.0	7	1	PPH2 LYCLES	P2518	DT 10-OCT-2003 (Rel. 42, Last annotation update)
3	16	34.0	8	1	AKH_LBAU	P2519	DE Leucokinin VII (L-VII)
4	16	34.0	8	1	NPMB_BOVIN	P2550	OS Leucophaea maderae (Madeira cockroach).
5	16	34.0	9	1	NEUD_COTMI	P2556	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaea.
6	15	31.9	4	1	OPC3_COTMI	P5849	NCBI_TaxID=6388
7	15	31.9	6	1	LOK1_LOCMI	P4149	RN [1] - RP TISSUE-read; RC Holman G.M., Cook B.J., Nachman R.J.; RT "Isolation, primary structure and synthesis of leucokinins VII and VIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae."; RT peptides isolated from head extracts of Leucophaea maderae.; RL Comp. Biochem. Physiol. 88C:31-34 (1987).
8	15	31.9	8	1	LCK1 LEUNA	P2114	CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile activity of cockroach protodeum (hindgut). CC -!- SUBCELLULAR LOCATION: Secreted.
9	15	31.9	8	1	LCK2 LEUNA	P2114	DR JS0318; JS0318.
10	15	31.9	8	1	LCK3 LEUNA	P2114	KW Neuropeptide; Amidation.
11	15	31.9	8	1	LCK4 LEUNA	P2114	FT MOD RES 8 8
12	15	31.9	8	1	LCK5 LEUNA	P1998	FT SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;
13	15	31.9	8	1	LCK6 LEUNA	P1998	Query Match 38.3%; Score 18; DB 1; Length 8;
14	15	31.9	8	1	LCK7 LEUNA	P1998	Best Local Similarity 66.7%; Pred. No. 1.4e+05;
15	14	29.8	7	1	HY7_FIG	P0115	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
16	14	29.8	7	1	TY51_LITRA	QY 3 FSW 5	
17	14	29.8	8	1	CAD1_ENTFA	DB 5 YSW 7	
18	14	29.8	8	1	COW2_CONPU	PH2_LYCES	
19	14	29.8	9	1	FIIB_MACFNU	ID PH2_LYCES STANDARD; PRT; 7 AA.	
20	14	29.8	9	1	RT33_BOVIN	AC P83379;	
21	13	27.7	8	1	AKHG_GRYBII	DT 28-FEB-2003 (Rel. 41, Created)	
22	13	27.7	8	1	HTF2_PERAM	DT 28-FEB-2003 (Rel. 41, Last sequence update)	
23	12	25.5	5	1	PAP2_PARMA	DE Purple acid phosphatase LesP2 (BC 3.1.3.2) (Fragment).	
24	12	25.5	6	1	BI01_LITRU	OS Lycopersicon esculentum (Tomato).	
25	12	25.5	7	1	BRHP_CONIM	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
26	12	25.5	7	1	TPFY_PACDA	OC Spermato phyta; Magnoliophyta; eudicotyledons; asterids;	
27	12	25.5	8	1	AKH_TABAT	OC Lamiidae; Solanaeae; Solanaceae; Solanaceae; Solanaceae;	
28	12	25.5	8	1	HTF1_PERAM	NCBI_TaxID=4081;	
29	12	25.5	8	1	HTF1_TENM0	RN [1] - RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND GLYCOSYLATION.	
30	12	25.5	8	1	RT34_BOVIN	RP STRAIN=cv. Moneymaker; TISSUE=Seed;	
31	12	25.5	9	1	PTSP_BOINNO	RC MEDLINE=22361242; PubMed=12473124;	
32	12	25.5	9	1	BPP7_BOTIN	RX P30425 bothrops in	
33	11	23.4	8	1	ALL7_CARMA		

ALIGNMENTS

Result 1	LCK8 LEUNA	STANDARD;	PRT;	8 AA.
AC P1990;				
DT 01-FEB-1991 (Rel. 17, Created)				
DT 01-FEB-1991 (Rel. 17, Last sequence update)				
DT 10-OCT-2003 (Rel. 42, Last annotation update)				
DE Leucokinin VII (L-VII)				
OS Leucophaea maderae (Madeira cockroach).				
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;				
OC Blaberidae; Leucophaea.				
OX NCBI_TaxID=6388;				
RN [1] -				
RP SEQUENCE.				
RC TISSUE-read;				
RA Holman G.M., Cook B.J., Nachman R.J.;				
RT "Isolation, primary structure and synthesis of leucokinins VII and VIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae.";				
RT peptides isolated from head extracts of Leucophaea maderae.;				
RL Comp. Biochem. Physiol. 88C:31-34 (1987).				
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile activity of cockroach protodeum (hindgut).				
CC -!- SUBCELLULAR LOCATION: Secreted.				
DR JS0318; JS0318.				
KW Neuropeptide; Amidation.				
FT MOD RES 8 8				
FT SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;				
Query Match 38.3%; Score 18; DB 1; Length 8;				
Best Local Similarity 66.7%; Pred. No. 1.4e+05;				
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY 3 FSW 5				
DB 5 YSW 7				
RESULT 2				
PH2_LYCES				
ID PH2_LYCES STANDARD; PRT; 7 AA.				
AC P83379;				
DT 28-FEB-2003 (Rel. 41, Created)				
DT 28-FEB-2003 (Rel. 41, Last sequence update)				
DE Purple acid phosphatase LesP2 (BC 3.1.3.2) (Fragment).				
OS Lycopersicon esculentum (Tomato).				
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC Spermato phyta; Magnoliophyta; eudicotyledons; asterids;				
OC Lamiidae; Solanaeae; Solanaceae; Solanaceae; Solanaceae;				
NCBI_TaxID=4081;				
RN [1] -				
RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND GLYCOSYLATION.				
RP STRAIN=cv. Moneymaker; TISSUE=Seed;				
RC MEDLINE=22361242; PubMed=12473124;				
RX P30425 bothrops in				

RA Bozzo G.G.; Raghothama K.G.; Plaxton W.C.;
 RT "Purification and characterization of two secreted purple acid
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
 RT esculentum) cell cultures." (Rel. 14, Last sequence update)
 RT Eur. J. Biochem. 269:6278-6286 (2002).
 RL CATALYTIC ACTIVITY: An orthophosphoric monoester + H₂O = an
 CC alcohol + phosphate.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: Glycosylated.
 CC -!- MISCELLANEOUS: In L.esculentum there are at least two isozymes of
 CC purple acid phosphatase.
 KW Hydrolase; Glycoprotein.
 FT² NON-TER¹
 FT² PT¹
 SQ SEQUENCE 7 AA; 810 MW; 672RA862C9CT29A0 CRC64;
 Query Match 34.0%; Score 16; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLF 3
 Db 1 FLF 3
 RESULT 3
 AKH_LIBAU ID AKH_LIBAU STANDARD; PRT; 8 AA.
 AC P25418;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 42, Last sequence update)
 DE Adiopokinetic hormone (AKH).
 OS Libellula auripennis (Skimmer dragonfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
 OX NCBI_TAXID=6966;
 RN [1] _TAXID=6966;
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90359055; PubMed=2390213;
 RA Gaede G.;
 RT "The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone family isolated and sequenced from a dragonfly." ;
 RL Biol. Chem. Hoppe-Seyler 371:475-483 (1990).
 CC -!- FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; S1096; S10596.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;
 Query Match 34.0%; Score 16; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Morphine modulating neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1] _TAXID=9913;
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RX MEDLINE=86067985; PubMed=3865193;
 RA Yang H.-Y.T.; Fratta W.; Mariani E.A.; Costa E.;
 RT "Isolation, sequencing, synthesis, and pharmacological characterization of two brain neuropeptides that modulate the action of morphine." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761 (1985).
 CC -!- FUNCTION: Modulates the action of morphine.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; B24749; B24749.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;
 Query Match 34.0%; Score 16; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLF 3
 Db 1 FLF 3
 RESULT 5
 NEUU_CAVPO ID NEUU_CAVPO STANDARD; PRT; 9 AA.
 AC P34976;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DR 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuromedin U-9 (NmU-9).
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TAXID=10141;
 RN [1] _TAXID=10141;
 RP SEQUENCE.
 RC TISSUE=small intestine;
 RX MEDLINE=90341105; PubMed=2381877;
 RA Murphy R.; Turner C.A.; Furness J.B.; Parker L.; Giraud A.;
 RT "Isolation and microsequence analysis of a novel form of neuromedin U from guinea pig small intestine." ;
 RL Peptides 11:613-617 (1990).
 CC -!- FUNCTION: Stimulates uterine smooth muscle contraction and causes selective vasoconstriction.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the NmU family.
 DR InterPro; IPR008199; NmU.
 DR Pfam; PF02070; NmU; 1.
 DR PROSITE; PS00967; NmU; 1.
 DR MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1169 MW; 1EFC177409C729DB CRC64;
 Query Match 34.0%; Score 16; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLFSW 5
 Db 4 FPTSW 8
 RESULT 4
 NPMB_BOVIN ID NPMB_BOVIN STANDARD; PRT; 8 AA.

Db	3	ELF 5	Query Match	31.9%	Score 15;	DB 1;	Length 6;
RESULT 6			Best Local Similarity	100.0%	Pred. No. 1.4e+05;		
OCP3_OCTMI		STANDARD;	Matches	2;	Conservative	0;	Indels 0;
ID	OCP3_OCTMI	PRT;	Gaps	0;			
AC	P58649;						
DT	28-FEB-2003 (Rel. 41, Created)	4 AA.					
DT	28-FEB-2003 (Rel. 41, Last sequence update)						
DE	Cardioactive Peptides Ocp-3/Ocp-4.						
OS	Octopus minor (Octopus).						
OC	Octopodiformes: Octopoda; Incirrata; Octopodidae; Octopus.						
NCBI_TaxID	89766;						
RN							
RP	SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.						
RC	TISSUE=Brain;						
RX	MEDLINE=20336B15; PubMed=10876044;						
RX	PubChem: 21336B15;						
RA	Iwakoshi E.; Hisada M.; Minakata H.;						
RA	"Cardioactive peptides isolated from the brain of a Japanese octopus, Octopus minor.,"						
RT	Peptides 21:622-630(2000).						
CC	-!- FUNCTION: Cardiactive; has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less active than Ocp-3.						
CC	-!- SUBCELLULAR LOCATION: Secreted.						
CC	-!- PTM: Ocp-4 has D-Ser instead of L-Ser.						
CC	-!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.						
KW	Hormone; D-amino acid.						
PT	MOD RES 2 2 2	D-SERTINE (IN OCP-4)					
SQ	SEQUENCE 4 AA; 463 MW;	GAB365810000000 CRC64;					
Query Match	31.9%	Score 15;	DB 1;	Length 4;			
Best Local Similarity	100.0%	Pred. No. 1.4e+05;					
Matches	2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	4 SW 5						
Db	2 SW 3						
RESULT 7			Query Match	31.9%	Score 15;	DB 1;	Length 8;
LOKI_LOCMI	LOKI_LOCMI	STANDARD;	Best Local Similarity	100.0%	Pred. No. 1.4e+05;	Matches 2;	Conservative 0;
ID	LOKI_LOCMI	PRT;	Mismatches 0;	Indels 0;	Gaps 0;		
AC	P41491;						
DT	01-NOV-1995 (Rel. 32, Created)	6 AA.					
DT	01-NOV-1995 (Rel. 32, Last sequence update)						
DE	Locustakinin I.						
OS	Locusta migratoria (Migratory locust).						
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; Acridoidea; Acridiidae; Oedipodinae; Locusta.						
NCBI_TaxID	7004;						
RP	SEQUENCE=Corpora cardiaca;						
RC	TISSUE=Head;						
RX	MEDLINE=9262851; PubMed=1585017;						
RA	Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K., de Loof A.;						
RT	"Locustakinin", novel myotropic peptide from <i>Locusta migratoria</i> , isolation, primary structure and synthesis.,"						
RT	Regul. Pept. 37:49-57(1992)						
CC	-!- FUNCTION: Myotropic peptide. May be important in the stimulation of ion transport and inhibition of diuretic activity in Malpighian tubules.						
CC	-!- SUBCELLULAR LOCATION: Secreted.						
DR	Neuropeptide; Amidation.						
PT	MOD RES 6	AMIDATION.					
SQ	SEQUENCE 6 AA; 654 MW;	686365A5B9CD0000 CRC64;					
Qy	4 SW 5						
Db	6 SW 3						
RESULT 8			Query Match	31.9%	Score 15;	DB 1;	Length 8;
LCK1_LEUMA	LCK1 LEUMA	STANDARD;	Best Local Similarity	100.0%	Pred. No. 1.4e+05;	Matches 2;	Conservative 0;
ID	P21140;	PRT;	Mismatches 0;	Indels 0;	Gaps 0;		
AC	P21140;						
DT	01-MAY-1991 (Rel. 18, Created)	8 AA.					
DT	10-OCT-2003 (Rel. 42, Last sequence update)						
DB	Leucophphaea maderae (Madeira cockroach).						
OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophphaea.						
NCBI_TaxID	6988;						
[1]	SEQUENCE, AND SYNTHESIS.						
PA	Holman G.M., Cook B.J., Nachman R.J.,						
RT	"Isolation, primary structure and synthesis of two neuropeptides from Leucophphaea maderae: members of a new family of Cephalomyotropins."						
RT	Comp. Biochem. Physiol. 84C:205-211(1986).						
RL	-!- FUNCTION: This cephalomyotropic peptide stimulates contractile activity of cockroach proctodeum (hindgut).						
CC	-!- SUBCELLULAR LOCATION: Secreted.						
KW	Neuropeptide; Amidation.						
FT	MOD RES 8	AMIDATION.					
SQ	SEQUENCE 8 AA; 893 MW;	DC6365B449CD76A CRC64;					
Qy	4 SW 5						
Db	6 SW 7						
RESULT 9			Query Match	31.9%	Score 15;	DB 1;	Length 8;
LCK2_LEUMA	LCK2 LEUMA	STANDARD;	Best Local Similarity	100.0%	Pred. No. 1.4e+05;	Matches 2;	Conservative 0;
ID	P21141;	PRT;	Mismatches 0;	Indels 0;	Gaps 0;		
AC	P21141;						
DT	01-MAY-1991 (Rel. 18, Created)	8 AA.					
DT	10-OCT-2003 (Rel. 42, Last sequence update)						
DB	Leucophphaea maderae (Madeira cockroach).						
OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophphaea.						
NCBI_TaxID	6388;						
[1]	SEQUENCE, AND SYNTHESIS.						
PA	Holman G.M., Cook B.J., Nachman R.J.,						
RT	"Isolation, primary structure and synthesis of two neuropeptides from Leucophphaea maderae: members of a new family of Cephalomyotropins."						
RT	Comp. Biochem. Physiol. 84C:205-211(1986).						
RL	-!- FUNCTION: This cephalomyotropic peptide stimulates contractile activity of cockroach proctodeum (hindgut).						
CC	-!- SUBCELLULAR LOCATION: Secreted.						
KW	Neuropeptide; Amidation.						
FT	MOD RES 8	AMIDATION.					
SQ	SEQUENCE 8 AA; 852 MW;	DC6365A5B9C8676A CRC64;					
Qy	4 SW 5						
Db	6 SW 7						

Query Match	31.9%;	Score 15;	DB 1;	Length 8;		
Best Local Similarity	100.0%;	Pred. No. 1.4e+05;				
Matches 2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	4 SW 5					
Db	6 SW 7					
RESULT 10						
LCK3 LEUMA	STANDARD;	PRT;	8 AA.			
AC P21142;						
DT 01-MAY-1991 (Rel. 1B, Created)						
DT 01-MAY-1991 (Rel. 1B, Last sequence update)						
DT 10-OCT-2003 (Rel. 42, Last annotation update)						
DE Leucokinin III (L-III).						
OS Leucophaeaa maderae (Madeira cockroach).						
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaeaa.						
NCBI_TAXID=6988;						
RN [1]						
RP SEQUENCE, AND SYNTHESIS.						
RC TISSUE=Head;						
RA Holman G.M., Cook B.J., Nachman R.J.;						
RT "Primary structure and synthesis of two additional neuropeptides from Leucophaeaa maderae: members of a new family of Cephalomyotropins."						
RL Comp. Biochem. Physiol. 94C:271-276(1986).						
CC -!- FUNCTION: This cephalomyotropin peptide stimulates contractile activity of cockroach protodeum (hindgut).						
CC -!- SUBCELLULAR LOCATION: Secreted.						
KW Neuropeptide; Amidation.						
FT MOD RES 8 B						
SQ AMIDATION.						
SEQUENCE 8 AA;	910 MW;	DC3635BA49C866DA CRC64;				
Query Match	31.9%;	Score 15;	DB 1;	Length 8;		
Best Local Similarity	100.0%;	Pred. No. 1.4e+05;				
Matches 2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	4 SW 5					
Db	6 SW 7					
RESULT 11						
LCK4 LEUMA	STANDARD;	PRT;	8 AA.			
AC P21143;						
DT 01-MAY-1991 (Rel. 1B, Created)						
DT 01-MAY-1991 (Rel. 1B, Last sequence update)						
DT 10-OCT-2003 (Rel. 42, Last annotation update)						
DE Leucokinin IV (L-IV).						
OS Leucophaeaa maderae (Madeira cockroach).						
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaeaa.						
NCBI_TAXID=6988;						
RN [1]						
RP SEQUENCE, AND SYNTHESIS.						
RC TISSUE=Head;						
RA Holman G.M., Cook B.J., Nachman R.J.;						
RT "Primary structure and synthesis of two additional neuropeptides from Leucophaeaa maderae: members of a new family of Cephalomyotropins."						
RL Comp. Biochem. Physiol. 84C:271-276(1986).						
CC -!- FUNCTION: This cephalomyotropin peptide stimulates contractile activity of cockroach protodeum (hindgut).						
CC -!- SUBCELLULAR LOCATION: Secreted.						
KW Neuropeptide; Amidation.						
FT MOD RES 8 B						
AMIDATION.						
SEQUENCE 8 AA;	784 MW;	736365A5B9C865DB CRC64;				
Query Match	31.9%;	Score 15;	DB 1;	Length 8;		
Best Local Similarity	100.0%;	Pred. No. 1.4e+05;				
Matches 2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	4 SW 5					
Db	6 SW 7					
RESULT 12						
LCK5 LEUMA	STANDARD;	PRT;	8 AA.			
AC P19987;						
DT 01-FEB-1991 (Rel. 17, Created)						
DT 01-FEB-1991 (Rel. 17, Last sequence update)						
DT 10-OCT-2003 (Rel. 42, Last annotation update)						
DE Leucokinin V (L-V).						
OS Leucophaeaa maderae (Madeira cockroach).						
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaeaa.						
NCBI_TAXID=6988;						
RN [1]						
RP SEQUENCE.						
RC TISSUE=Head;						
RA Holman G.M., Cook B.J., Nachman R.J.;						
RT "Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic peptides of Leucophaeaa maderae."						
RL Comp. Biochem. Physiol. 88C:27-30(1987).						
CC -!- FUNCTION: This cephalomyotropin peptide stimulates contractile activity of cockroach protodeum (hindgut).						
CC -!- SUBCELLULAR LOCATION: Secreted.						
KW ACTIVITY OF COCKROACH PROTODEUM.						
FT MOD RES 8 B						
AMIDATION.						
SEQUENCE 8 AA;	736365A5B9C865DB CRC64;					
Query Match	31.9%;	Score 15;	DB 1;	Length 8;		
Best Local Similarity	100.0%;	Pred. No. 1.4e+05;				
Matches 2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	4 SW 5					
Db	6 SW 7					
RESULT 13						
LCK6 LEUMA	STANDARD;	PRT;	8 AA.			
AC P19988;						
DT 01-FEB-1991 (Rel. 17, Created)						
DT 01-FEB-1994 (Rel. 28, Last sequence update)						
DT 10-OCT-2003 (Rel. 42, Last annotation update)						
DE Leucokinin VI (L-VI).						
OS Leucophaeaa maderae (Madeira cockroach).						
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaeaa.						
NCBI_TAXID=6988;						
RN [1]						
RP SEQUENCE.						
RC TISSUE=Head;						
RA Holman G.M., Cook B.J., Nachman R.J.;						
RT "Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic peptides of Leucophaeaa maderae."						
RL Comp. Biochem. Physiol. 88C:27-30(1987).						
CC -!- FUNCTION: This cephalomyotropin peptide stimulates contractile activity of cockroach protodeum (hindgut).						
CC -!- SUBCELLULAR LOCATION: Secreted.						
KW ACTIVITY OF COCKROACH PROTODEUM.						
FT MOD RES 8 B						

DR PIR; JS0316; JS0316
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT 1
 MOD RES 1 AMIDATION
 FT 8 PYRROLIDONE CARBOXYLIC ACID.
 SQ 8 AA; 935 MW; 906365B1E9D5A5A6 CRC64;

Query Match 31.9%; Score 15; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 SW 5
 Db 6 SW 7

DR PIR; A01417; NYPG7;
 SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;
 Query Match 29.8%; Score 14; DB 1; Length 7;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FLFSWY 6
 Db 1 FIVHSY 6

Search completed: March 18, 2004, 13:35:31
 Job time : 12 secs

RESULT 14

LCK7 LEUMA STANDARD PRT; 8 AA.
 ID LCK7 LEUMA
 AC P1989;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 LEUCOKININ VII (L-VII)
 OS Leucophaga maderae (Madeira Cockroach)
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaga;
 OX NCBI_TaxID=6988;
 RN [1]

SEQUENCE
 RC TISSUE=Head;
 RA Holman G. M., Cook B. J., Nachman R. J.;
 RT "Isolation, primary structure and synthesis of leucokinins VII and
 VIII: the final members of this new family of cephalomyotropin
 peptides isolated from head extracts of Leucophaga maderae.";
 RL Comp. Biochem. Physiol. 88C:31-34 (1987).
 CC -!- FUNCTION: This cephalomyotropin peptide stimulates contractile
 activity of cockroach proctodeum (hindgut).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; JS0317; JS0317.
 KW Neuropeptide; Amidation.
 FT 8 AMIDATION
 MOD RES 8
 SQ 8 AA; 666 MW; 906365A5B9CD76A CRC64;

Query Match 31.9%; Score 15; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 SW 5
 Db 6 SW 7

RESULT 15

HY7 PIG STANDARD PRT; 7 AA.
 ID HY7 PIG
 AC P01153;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 OS Hypothalamic heptapeptide.
 OC Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN NCBI_TaxID=9823;
 RN SEQUENCE AND SYNTHESIS.
 RP MEDLINE=1213980; PubMed=6261778;
 RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
 RA Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
 RT "Isolation, structure and synthesis of a heptapeptide with *in vitro*
 ACTH-releasing activity from porcine hypothalamus.";
 RT Horm. Metab. Res. 13:228-232 (1981).
 RL

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:32:50 ; Search time 38 Seconds

Perfect score: 47
 Sequence: 1 FLFSWVAXV 9

Title: US-09-920-480B-3

Scoring table: BLOSUM62
 Gapext 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 840
 Minimum DB seq length: 0
 Maximum DB seq length: 9

Posit-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : SPTREMBL 25:
 1: sp_archea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_nhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_rvirus:
 16: sp_bacteriap:
 17: sp_archaeap:
 18: sp_archeap:
 19: sp_bacteria:
 20: sp_fungi:
 21: sp_invertebrate:
 22: sp_mammal:
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 748: sp_virus:
 749: sp_vertebrate:
 750: sp_unclassified:
 751: sp_rvirus:
 752: sp_bacteriap:
 753: sp_archeap:
 754: sp_bacteria:
 755: sp_fungi:
 756: sp_invertebrate:
 757: sp_mammal:
 758: sp_nhc:
 759: sp_organelle:
 760: sp_phage:
 761: sp_plant:
 762: sp_rabbit:
 763: sp_virus:
 764: sp_vertebrate:
 765: sp_unclassified:
 766: sp_rvirus:
 767: sp_bacteriap:
 768: sp_archeap:
 769: sp_bacteria:
 770: sp_fungi:
 771: sp_invertebrate:
 772: sp_mammal:
 773: sp_nhc:
 774: sp_organelle:
 775: sp_phage:
 776: sp_plant:
 777: sp_rabbit:
 778: sp_virus:
 779: sp_vertebrate:
 780: sp_unclassified:
 781: sp_rvirus:
 782: sp_bacteriap:
 783: sp_archeap:
 784: sp_bacteria:
 785: sp_fungi:
 786: sp_invertebrate:
 787: sp_mammal:
 788: sp_nhc:
 789: sp_organelle:
 790: sp_phage:
 791: sp_plant:
 792: sp_rabbit:
 793: sp_virus:
 794: sp_vertebrate:
 795: sp_unclassified:
 796: sp_rvirus:
 797: sp_bacteriap:
 798: sp_archeap:
 799: sp_bacteria:
 800: sp_fungi:
 801: sp_invertebrate:
 802: sp_mammal:
 803: sp_nhc:
 804: sp_organelle:
 805: sp_phage:
 806: sp_plant:
 807: sp_rabbit:
 808: sp_virus:
 809: sp_vertebrate:
 810: sp_unclassified:
 811: sp_rvirus:
 812: sp_bacteriap:
 813: sp_archeap:
 814: sp_bacteria:
 815: sp_fungi:
 816: sp_invertebrate:
 817: sp_mammal:
 818: sp_nhc:
 819: sp_organelle:
 820: sp_phage:
 821: sp_plant:
 822: sp_rabbit:
 823: sp_virus:
 824: sp_vertebrate:
 825: sp_unclassified:
 826: sp_rvirus:
 827: sp_bacteriap:
 828: sp_archeap:
 829: sp_bacteria:
 830: sp_fungi:
 831: sp_invertebrate:
 832: sp_mammal:
 833: sp_nhc:
 834: sp_organelle:
 835: sp_phage:
 836: sp_plant:
 837: sp_rabbit:
 838: sp_virus:
 839: sp_vertebrate:
 840: sp_unclassified:
 841: sp_rvirus:
 842: sp_bacteriap:
 843: sp_archeap:
 844: sp_bacteria:
 845: sp_fungi:
 846: sp_invertebrate:
 847: sp_mammal:
 848: sp_nhc:
 849: sp_organelle:
 850: sp_phage:
 851: sp_plant:
 852: sp_rabbit:
 853: sp_virus:
 854: sp_vertebrate:
 855: sp_unclassified:
 856: sp_rvirus:
 857: sp_bacteriap:
 858: sp_archeap:
 859: sp_bacteria:
 860: sp_fungi:
 861: sp_invertebrate:
 862: sp_mammal:
 863: sp

RESULT 2	Q94VF6	PRELIMINARY;	PRT;	8 AA.	
Qy	1 FLPFWYAXY 9 : 1 FQPFWEVIV 9				9 AA.
Db	AC Q94VF6; ID 01-DEC-2001 (TREMBLrel. 19, Created) DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
	DE Cytochrome c oxidase subunit I (Fragment).				
	GN COI.				
	OS Varanus jobiensis (Peach throat monitor).				
	OG Mitochondrion.				
	BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauaria; Squamata; Scierioglossa; Anguimorpha; Varanidae; Varanus.				
	NCBI_TaxID=169843;				
	RP SEQUENCE FROM N.A.				
	RA Ast J.C.;				
	RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata)."; Cladistics 17:0-0 (2001).				
	RL EMBL: AF407507; AAL10075.1; -.				
	DR GO: 00005339; C:mitochondrion; IEA.				
	KW Mitochondrion.				
	FT NON_TER 8 SEQUENCE 8 AA; 1144 MW;	Score 18; Best Local Similarity 100.0%; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DB 4; Pred. No. 1e+06;	Length 8; Score 18; Best Local Similarity 100.0%; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	Qy 5 WY 6 Db 4 WY 5				
	RESULT 3				
	Q9UK44	PRELIMINARY;	PRT;	9 AA.	
	AC Q9UK44; ID 01-MAY-2000 (TREMBLrel. 13, Created)				
	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
	DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)				
	DE Signal transducer and activator of transcription 1 (Fragment).				
	GN STAT1.				
	OS Homo sapiens (Human).				
	OC BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.				
	NCBI_TaxID=9606;				
	RP SEQUENCE FROM N.A.				
	RA Wong L.H., Sim H., Hatzinikolou I., Ralph S.J.;"STARI human genomic 5' Intron 1."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.				
	RL EMBL: AF182314; AAC04559.1; -.				
	DR EFT NON_TER 9 SEQUENCE 9 AA; 1212 MW;	Score 18; Best Local Similarity 100.0%; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DB 4; Pred. No. 1e+06;	Length 9; Score 18; Best Local Similarity 100.0%; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	Qy 5 WY 6 Db 4 WY 5				
	RESULT 4				
	PB2685	PRELIMINARY;	PRT;	8 AA.	
	AC PB2685; ID 01-MAR-2001 (TREMBLrel. 16, Created)				
	DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
	DE Kinin-1 (PEA-K-1).				
	OS Periplaneta americana (American cockroach).				
	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.				
	OC NCBI_TaxID=6378;				
	RP SEQUENCE, AND FUNCTION.				
	RC TISSUE=CORPORA CARDIACA.				
	RT MEDLINE=98010462; PubMed=9150979;				
	RA Prede R., Kellner R., Rapus J., Penzlin H., Gaede G.;				
	RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, <i>Periplaneta americana</i> .";				
	RT Regul. Pept. 71:199-205 (1997).				
	CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MOTOTROPIC ACTIVITY).				
	CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.				
	CC GO: 00007218; P:neuropeptide signaling pathway; IEA.				
	KW Neuropeptide; Amidation.				
	FT MOD_RES 8 SEQUENCE 8 AA; 950 MW;	AMIDATION.			
	SQ 326365B44D5A774 CRC64;				
	Query Match 4 SW 5 Db 6 SW 7				
	RESULT 5				
	PB2685	PRELIMINARY;	PRT;	8 AA.	
	AC PB2685; ID 01-MAR-2001 (TREMBLrel. 16, Created)				
	DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
	DE Kinin-1 (PEA-K-1).				
	OS Periplaneta americana (American cockroach).				
	OC Eukaryota; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.				
	OC NCBI_TaxID=6378;				
	RP SEQUENCE, AND FUNCTION.				
	RC TISSUE=CORPORA CARDIACA.				
	RT MEDLINE=98010462; PubMed=9150979;				
	RA Prede R., Kellner R., Rapus J., Penzlin H., Gaede G.;				
	RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, <i>Periplaneta americana</i> .";				
	RT Regul. Pept. 71:199-205 (1997).				
	CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MOTOTROPIC ACTIVITY).				
	CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.				
	CC GO: 00007218; P:neuropeptide signaling pathway; IEA.				
	KW Neuropeptide; Amidation.				
	FT MOD_RES 8 SEQUENCE 8 AA; 950 MW;	AMIDATION.			
	SQ 326365B44D5A774 CRC64;				
	Query Match 4 SW 5 Db 6 SW 7				
	RESULT 6				
	PB2686	PRELIMINARY;	PRT;	8 AA.	
	AC PB2686; ID 01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
	DE 28 kDa heat shock protein homolog fragment 1 (Fragment).				
	OS Homo sapiens (Human).				
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.				
	NCBI_TaxID=9606;				
	RP SEQUENCE FROM N.A.				
	RA Wong L.H., Sim H., Hatzinikolou I., Ralph S.J.;"STARI human genomic 5' Intron 1."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.				
	RL EMBL: AF182314; AAC04559.1; -.				
	DR EFT NON_TER 9 SEQUENCE 9 AA; 1212 MW;	Score 18; Best Local Similarity 100.0%; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DB 4; Pred. No. 1e+06;	Length 9; Score 18; Best Local Similarity 100.0%; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	Qy 5 WY 6 Db 4 WY 5				

AC P82686;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Kinin-2 (PEA-K-2)
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RT "Isolation and structural elucidation of eight kinins from the
 retrocerebral complex of the American cockroach, *Periplaneta
 americana*."
 RL Regul. Pept. 71:199-205 (1997).
 CC |- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC |- SIMILARITY: BELONGS TO THE KININ FAMILY.
 DR GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION
 SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D8D2A CRC64;
 Query Match 31.9%; Score 15; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OX ;
 OX ;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RT "Isolation and structural elucidation of eight kinins from the
 retrocerebral complex of the American cockroach, *Periplaneta
 americana*."
 RL Regul. Pept. 71:199-205 (1997).
 CC |- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC |- SIMILARITY: BELONGS TO THE KININ FAMILY.
 DR GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION
 SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D8D2A CRC64;
 Query Match 31.9%; Score 15; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OX ;
 OX ;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RT "Isolation and structural elucidation of eight kinins from the
 retrocerebral complex of the American cockroach, *Periplaneta
 americana*."
 RL Regul. Pept. 71:199-205 (1997).
 CC |- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC |- SIMILARITY: BELONGS TO THE KININ FAMILY.
 DR GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION
 SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D8D2A CRC64;
 Query Match 31.9%; Score 15; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches	2;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	Qy	1 FLFS 4
Qy	4 SW 5									Db	1 : 7
Db	6 SW 7									Db	4 WLFS 7
RESULT 10											
QBWGD7	PRELIMINARY;	PRT;	8 AA.							Q9T4Y2	PRELIMINARY;
AC	QBWGD7;									AC	Q9T4Y2;
DT	01-MAR-2002	(TREMBLrel.	20,	Created)						DT	01-MAY-2000 (TREMBLrel.
DT	01-MAR-2002	(TREMBLrel.	20,	Last sequence update)						DT	13, Last sequence update)
DT	01-JUN-2003	(TREMBLrel.	24,	Last annotation update)						DT	01-JUN-2003 (TREMBLrel.
DE	Cytochrome oxidase subunit 1	(Fragment).								DE	COI gene Product (Fragment).
OS	Lomis hirta.									OS	Asteririna pectinifera (Starfish).
OG	Mitochondrion.									OG	Mitochondrion.
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Bivalvata; Valvatida; Asterinida; Asterozoa;									OC	Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa; Asterinida; Asterina.
OC	Bivalvata; Eumalacostraca; Decapoda; Pleocyemata; Anomura; Lomoidea;									OC	Asterozoa; Valvatida; Valvatida; Asterinida; Asterina.
OC	Lomidae; Lonidae.									OC	NCBI_TaxID=7594;
OX	NCBI_TaxID=177234;									OX	SEQUENCE FROM N.A.
RN										RP	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.									RX	MEDLINE:89354665; PubMed:2766382;
RA	MORRISON C.L.; Harvey A.W., Lavery S., Tieu K., Huang Y., Cunningham C.W.;									RA	Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
RA	"Mitochondrial gene rearrangements support a hypothesis of parallel evolution to the crab-like form."									RA	"Conserved tRNA gene cluster in starfish mitochondrial DNA."
RT	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.									RT	Curc Genet. 15:193-206 (1989).
RT	EMBL: AF430535; AAL31611.1;									RT	EMBL: X16886; CAA34767.1;
RT	GO: GO:0005739; C:mitochondrion; IEA.									RT	GO: GO:0005739; C:mitochondrion; IEA.
DR	Mitochondrion.									DR	Mitochondrion.
FT	NON-TER 1	1								FT	NON-TER 8
FT	NON-TER 8	8								FT	NON-TER 8
SEQUENCE	8 AA;	1038 MW;								SEQUENCE	8 AA;
SQ	C585B9C733640321 CRC64;									SQ	1114 MW;
Query Match	31.9%	Score 15;	DB 8;	Length 8;						Query Match	31.9%
Best Local Similarity	75.0%	Pred. No. 1e+06;								Best Local Similarity	40.0%
Matches	3;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	Matches	2;
Qy	1 FLFS 4									Qy	2 LFWSWY 6
Db	1 :									Db	3 LSRWFW 7
RESULT 11											
Q94V88	PRELIMINARY;	PRT;	8 AA.							Q94V74	PRELIMINARY;
AC	Q94V88;									AC	Q94V74;
DT	01-DEC-2001	(TREMBLrel.	19,	Created)						DT	01-DEC-2001 (TREMBLrel.
DT	01-DEC-2001	(TREMBLrel.	19,	Last sequence update)						DT	19, Last sequence update)
DT	01-JUN-2003	(TREMBLrel.	24,	Last annotation update)						DT	01-JUN-2003 (TREMBLrel.
DE	Cytochrome c oxidase subunit I (Fragment).									DE	Cytochrome c oxidase subunit I (Fragment).
GN										GN	COI.
OS	Varanus bengalensis nebulosus (Clouded monitor).									OS	Varanus bengalensis nebulosus (Clouded monitor).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.									OC	Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OG	Varanus tristis.									OG	NCBI_TaxID=169827;
OC	Mitochondrion.									OC	Mitochondrion.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.									OC	NCBI_TaxID=62052;
OX	NCBI_TaxID=1041 MW;									OX	SEQUENCE FROM N.A.
RN										RN	AST J.C.;
RP	SEQUENCE FROM N.A.									RP	"Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RA										RA	Cladistics 17:0-0(2001);
RA	"Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";									RA	EMBL: AF407492; AA10031.1;
RA	Cladistics 17:0-0(2001).									RA	GO: GO:0005739; C:mitochondrion; IEA.
RL	Cladistics 17:0-0(2001).									RL	Mitochondrion.
DR	GO: GO:0005739; C:mitochondrion; IEA.									DR	GO: GO:0005739; C:mitochondrion; IEA.
KW	Mitochondrion.									KW	Mitochondrion.
FT	NON-TER 8	8								FT	NON-TER 8
SEQUENCE	8 AA;	1041 MW;								SEQUENCE	8 AA;
SQ	B885B9C7336411A6 CRC64;									SQ	1053 MW;
Query Match	31.9%	Score 15;	DB 8;	Length 8;						Query Match	31.9%
Best Local Similarity	75.0%	Pred. No. 1e+06;								Best Local Similarity	75.0%
Matches	3;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	Matches	3;
Qy	1 FLFS 4									Qy	1 FLFS 4
Db	1 :									Db	4 WLFS 7

RESULT 14

Q94V91	PRELIMINARY;	PRT;	8 AA.
ID Q94V91;			
AC Q94V91;			
DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE Cytochrome c oxidase subunit I (Fragment).			
GN COI.			
OS Varanus timorensis (Timor monitor).			
OG Mitochondrion.			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.			
OX NCBI_TaxID=62053;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Ast J.C.;			
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata)." ;			
RL Cladistics 17:0-0 (2001).			
DR EMBL; AF407532; AAL10148.1; -.			
DR GO:0005739; C-mitochondrion; IEA.			
KW Mitochondrion.			
FT NON_TER 8 8			
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;			
Qy 1 FLFS 4			
Db 4 WLFS 7			

RESULT 15

Q94V94	PRELIMINARY;	PRT;	8 AA.
ID Q94V94;			
AC Q94V94;			
DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DB Cytochrome c oxidase subunit I (Fragment).			
GN COI.			
OS Varanus melinus (Quince monitor lizard).			
OG Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.			
OX NCBI_TaxID=169846;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Ast J.C.;			
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata)." ;			
RL Cladistics 17:0-0 (2001).			
DR EMBL; AF407511; AAL10087.1; -.			
DR GO:0005739; C-mitochondrion; IEA.			
KW Mitochondrion.			
FT NON_TER 8 8			
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;			
Qy 1 FLFS 4			
Db 4 WLFS 7			

CC expressing cell surface tumour antigen. They are also useful in a variety
 CC of methods of modulating an immune response to the synthetic antigenic
 CC peptide epitopes and thus to the corresponding native antigenic
 CC determinant. The synthetic antigenic peptide epitopes find application in
 CC a wide variety of immunomodulatory protocols, including methods to induce
 CC or increase an immune response, as well as in methods to suppress or
 CC reduce an undesirable immune response to a corresponding natural epitope
 XX

Sequence 9 AA;

Query Match 95.7%; Score 45; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 AAY84757

QY 1 FLFSWYAXV 9
 Db 1 FLFSWYAXV 9

RESULT 2
 AAY84756

ID AAY84756 standard; peptide; 9 AA.

XX AC AAY84756;

XX DT 08-AUG-2000 (first entry)

XX DE Antigenic peptide epitope of insulin-like growth factor II receptor.

XX AC Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;

XX DT tumour antigen; vaccine; tumour cell; immune response.

XX OS Synthetic.

XX PN WO200020457-A1.

XX PR 08-AUG-2000

XX PD 13-APR-2000.

XX PF 04-OCT-1999; 99WO-US023167.

XX XX

XX PR 05-OCT-1998; 98US-0103229P.

XX PR 05-JAN-1999; 99US-0114811P.

XX PR 11-FEB-1999; 99US-0120001P.

XX PR 11-FEB-1999; 99US-0120002P.

XX XX

XX PA (GENZYME CORP.

XX XX

XX DR WPI; 2000-303749/26.

XX XX

XX PT New synthetic antigenic peptide epitopes related to insulin-like growth

XX PR factor receptor, useful as vaccines against tumor cells expressing cell

XX PR surface tumor antigen.

XX XX

XX PS Claim 3; Page 91; 116pp; English.

XX XX

XX AAY84756-61 represent synthetic antigenic peptide epitopes of insulin-

CC like growth factor II receptor (IGF-II-R). The synthetic peptides bind to

CC a MHC class I or class II molecule with a higher affinity than the

CC natural sequence. The synthetic antigenic peptide epitopes may correspond

CC to tumour antigens, and are therefore useful as vaccines against tumour

CC cells expressing cell surface tumour antigen. They are also useful in a

CC variety of methods of modulating an immune response to the synthetic

CC antigenic peptide epitopes and thus to the corresponding native antigenic

CC determinant. The synthetic antigenic peptide epitopes find application in

CC a wide variety of immunomodulatory protocols, including methods to induce

CC or increase an immune response, as well as in methods to suppress or

CC reduce an undesirable immune response to a corresponding natural epitope

XX XX

XX Sequence 9 AA;

XX DR 2000-303749/26.

XX XX

XX PT New synthetic antigenic peptide epitopes related to insulin-like growth

CC factor receptor, useful as vaccines against tumor cells expressing cell

CC PR surface tumor antigen.

CC XX

CC PS Claim 1; Page 91; 116pp; English.

CC XX

CC PI Nicolette CA;

CC DR WPI; 2000-303749/26.

CC XX

CC PT New synthetic antigenic peptide epitopes may correspond

CC to tumour antigens, and are therefore useful as vaccines against tumour

CC cells expressing cell surface tumour antigen. They are also useful in a

CC variety of methods of modulating an immune response to the synthetic

CC antigenic peptide epitopes and thus to the corresponding native antigenic

CC determinant. The synthetic antigenic peptide epitopes find application in

CC a wide variety of immunomodulatory protocols, including methods to induce

CC or increase an immune response, as well as in methods to suppress or

CC reduce an undesirable immune response to a corresponding natural epitope

XX XX

XX Sequence 9 AA;

XX DR 2000-303749/26.

XX XX

XX PT New synthetic antigenic peptide epitopes bind to the corresponding native antigenic

CC determinant. The synthetic antigenic peptide epitopes find application in

CC a wide variety of immunomodulatory protocols, including methods to induce

CC or increase an immune response, as well as in methods to suppress or

CC reduce an undesirable immune response to a corresponding natural epitope

XX SQ Sequence 9 AA;

Query Match 95.7%; Score 45; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLFSWYAXV 9
 Db 1 FLFSWYAXV 9

RESULT 3
 AAY84757

XX ID AAY84757 standard; peptide; 9 AA.

XX AC AAY84757;

XX DT 08-AUG-2000 (first entry)

XX DE Antigenic peptide epitope of insulin-like growth factor II receptor.

XX KW Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;

XX KW tumour antigen; vaccine; tumour cell; immune response.

XX OS Synthetic.

XX PN WO200020457-A1.

XX PR 05-OCT-1998; 98US-0103229P.

XX PR 05-JAN-1999; 99US-0114811P.

XX PR 11-FEB-1999; 99US-0120001P.

XX PR 11-FEB-1999; 99US-0120002P.

XX XX

XX PA (GENZYME CORP.

XX XX

XX DR WPI; 2000-303749/26.

XX XX

XX PT New synthetic antigenic peptide epitopes related to insulin-like growth

CC factor receptor, useful as vaccines against tumor cells expressing cell

CC PR surface tumor antigen.

CC XX

CC PS Claim 3; Page 91; 116pp; English.

CC XX

CC AAY84756-61 represent synthetic antigenic peptide epitopes of insulin-

CC like growth factor II receptor (IGF-II-R). The synthetic peptides bind to

CC a MHC class I or class II molecule with a higher affinity than the

CC natural sequence. The synthetic antigenic peptide epitopes may correspond

CC to tumour antigens, and are therefore useful as vaccines against tumour

CC cells expressing cell surface tumour antigen. They are also useful in a

CC variety of methods of modulating an immune response to the synthetic

CC antigenic peptide epitopes and thus to the corresponding native antigenic

CC determinant. The synthetic antigenic peptide epitopes find application in

CC a wide variety of immunomodulatory protocols, including methods to induce

CC or increase an immune response, as well as in methods to suppress or

CC reduce an undesirable immune response to a corresponding natural epitope

CC XX

CC Sequence 9 AA;

Query Match 87.2%; Score 41; DB 3; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLFSWYAXV 9
 Db 1 FLFSWYAXV 9

RESULT 3
 AAY84757

XX ID AAY84757 standard; peptide; 9 AA.

XX AC AAY84757;

XX DT 08-AUG-2000 (first entry)

XX DE Antigenic peptide epitope of insulin-like growth factor II receptor.

XX KW Antigenic epitope; insulin-like growth factor II receptor; IGF-II-R;

XX KW tumour antigen; vaccine; tumour cell; immune response.

XX OS Synthetic.

XX PN WO200020457-A1.

XX PR 05-OCT-1998; 98US-0103229P.

XX PR 05-JAN-1999; 99US-0114811P.

XX PR 11-FEB-1999; 99US-0120001P.

XX PR 11-FEB-1999; 99US-0120002P.

XX XX

XX PA (GENZYME CORP.

XX XX

XX DR WPI; 2000-303749/26.

XX XX

XX PT New synthetic antigenic peptide epitopes related to insulin-like growth

CC factor receptor, useful as vaccines against tumor cells expressing cell

CC PR surface tumor antigen.

CC XX

CC PS Claim 3; Page 91; 116pp; English.

CC XX

CC AAY84756-61 represent synthetic antigenic peptide epitopes of insulin-

CC like growth factor II receptor (IGF-II-R). The synthetic peptides bind to

CC a MHC class I or class II molecule with a higher affinity than the

CC natural sequence. The synthetic antigenic peptide epitopes may correspond

CC to tumour antigens, and are therefore useful as vaccines against tumour

CC cells expressing cell surface tumour antigen. They are also useful in a

CC variety of methods of modulating an immune response to the synthetic

CC antigenic peptide epitopes and thus to the corresponding native antigenic

CC determinant. The synthetic antigenic peptide epitopes find application in

CC a wide variety of immunomodulatory protocols, including methods to induce

CC or increase an immune response, as well as in methods to suppress or

CC reduce an undesirable immune response to a corresponding natural epitope

XX	04-OCT-1999;	99WO-US023167.	PI	Nicolette CA;
PF			XX	
XX	05-OCT-1998;	98US-0103229P.	DR	WPI; 2000-303749/26.
PR	05-JAN-1999;	99US-0114811P.	XX	
PR	11-FEB-1999;	99US-0120001P.	PT	New synthetic antigenic peptide epitopes related to insulin-like growth
PR	11-FEB-1999;	99US-0120002P.	PT	factor receptor, useful as vaccines against tumor cells expressing cell
XX			PT	surface tumor antigen.
PA	(GENZ) GENZYME CORP.		XX	
PA			PS	Example 1; Page 85; 116pp; English.
XX			XX	
PI			CC	AAV84756-61 represent synthetic antigenic peptide epitopes of insulin-
NI			CC	like growth factor II receptor (IGF-II-R). The synthetic peptides bind to
XX			CC	a MHC class I or class II molecule with a higher affinity than the
DR			CC	natural sequence. The synthetic antigenic peptide epitopes may correspond
XX			CC	to tumour antigens, and are therefore useful as vaccines against tumour
WPI			CC	cells expressing cell surface tumour antigen. They are also useful in a
XX			CC	variety of methods of modulating an immune response to the synthetic
XX			CC	peptide epitopes and thus to the corresponding native antigenic
XX			CC	determinant. The synthetic antigenic peptide epitopes find application in
XX			CC	a wide variety of immunomodulatory protocols, including methods to induce
XX			CC	or increase an immune response, as well as in methods to suppress or
XX			CC	reduce an undesirable immune response to a corresponding natural epitope
PS			XX	Sequence 9 AA;
XX			XX	Query Match 74.5%; Score 35; DB 3; Length 9;
XX			XX	Best Local Similarity 83.3%; Pred. No. 1.4e+06;
XX			XX	Matches 1; Mismatches 0; Indels 0;
XX			Qy	1 FLFSW 6
XX			Db	:
XX			XX	1 YLFWSW 6

PT kidney diseases.
 XX Disclosure; Page 19; 89pp; English.
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 derived from the Chemotaxis Inhibitory Protein (CHIPS) from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

XX Sequence 6 AA;

Query Match 72.3%; Score 34; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLFSWY 6
 Db 1 FFFSWY 6

RESULT 9

ABR47094 ID ABR47094 standard; peptide; 6 AA.
 XX ABR47094; AC
 XX DT 10-JUN-2003 (first entry)
 DE Staphylococcus aureus CHIPS-related peptide #2284.

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiotonic; cerebroprotective; neuroprotective; nootropic; dermatological; synecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus. OS Synthetic.
 XX WO2003006048-A1. OS
 XX PD 23-JAN-2003. OS
 XX PF 11-JUL-2001; 2001WO-EP008004. OS
 XX PR 11-JUL-2001; 2001WO-EP008004. OS
 XX PA (JARI-) JARI PHARM BV. OS
 XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW; PI Van Strijp JAG; PI
 XX WO2003006048-A1. PI
 XX PD 23-JAN-2003. PI
 XX PF 11-JUL-2001; 2001WO-EP008004. PI
 XX PR 11-JUL-2001; 2001WO-EP008004. PI
 XX PA (JARI-) JARI PHARM BV. PI
 XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW; PI Van Strijp JAG; PI
 XX DR 2003-256333/25. PI
 XX DR WPI; 2003-256333/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases.

XX Disclosure; Page 19; 89pp; English.

CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 derived from the Chemotaxis Inhibitory Protein (CHIPS) from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

XX Sequence 6 AA;

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

XX Sequence 6 AA;

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

XX Sequence 6 AA;

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

XX Sequence 6 AA;

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

XX Sequence 6 AA;

Query Match 70.2%; Score 33; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLFSWY 6
 Db 1 FFFSWY 6

RESULT 10

ABR47052 ID ABR47052 standard; peptide; 6 AA.
 XX ABR47052; AC
 XX DT 10-JUN-2003 (first entry)

DE Staphylococcus aureus CHIPS-related peptide #2242.

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiotonic; cerebroprotective; neuroprotective; nootropic; dermatological; synecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus. OS Synthetic.

XX WO2003006048-A1. OS

XX PD 23-JAN-2003. OS

XX PF 11-JUL-2001; 2001WO-EP008004. OS

XX PR 11-JUL-2001; 2001WO-EP008004. OS

XX PA (JARI-) JARI PHARM BV. OS

XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW; PI Van Strijp JAG; PI

XX DR WPI; 2003-256333/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases.

XX Disclosure; Page 19; 89pp; English.

CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 derived from the Chemotaxis Inhibitory Protein (CHIPS) from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

XX Sequence 6 AA;

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

XX Sequence 6 AA;

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

XX Sequence 6 AA;

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

XX Sequence 6 AA;

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

XX Sequence 6 AA;

DT 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #2283.
 XX
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 XX formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 XX inflammation; cardiovascular disease; central nervous system disease;
 XX gastrointestinal disease; skin disease; genitourinary disease;
 XX joint disease; respiratory disease; HIV infection; antiinflammatory;
 XX cardiant; cerebroprotective; nootropic; dermatological;
 XX synecological; immunosuppressive; anti-HIV.
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 XX WO2003006048-A1.
 XX
 XX PD 23-JAN-2003.
 XX PF 11-JUL-2001; 2001WO-EP008004.
 XX PR 11-JUL-2001; 2001WO-EP008004.
 XX
 XX (JARI-) JARI PHARM BV.
 XX
 XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 XX DR WPI; 2003-256333/25.
 XX
 XX PT Combination of peptides derived from chemotaxis inhibiting protein from
 XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 XX prophylaxis and/or treatment of inflammation, cardiovascular, skin and
 XX kidney diseases.
 XX
 XX Disclosure; Page 19; 89pp; English.
 XX
 XX DR WPI; 2003-256333/25.
 XX
 XX PT Combination of peptides derived from chemotaxis inhibiting protein from
 XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 XX prophylaxis and treatment of inflammation, cardiovascular, skin and
 XX kidney diseases.
 XX
 XX PT (JARI-) JARI PHARM BV.
 XX
 XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 XX PR 11-JUL-2001; 2001WO-EP008004.
 XX
 XX (JARI-) JARI PHARM BV.
 XX
 XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 XX DR WPI; 2003-256333/25.
 XX
 XX PT Combination of peptides derived from chemotaxis inhibiting protein from
 XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 XX prophylaxis and treatment of inflammation, cardiovascular, skin and
 XX kidney diseases.
 XX
 XX PT (JARI-) JARI PHARM BV.
 XX
 XX Disclosure; Page 19; 89pp; English.
 XX
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 CC Sequence 6 AA;
 XX
 XX Query Match 68.1%; Score 32; DB 6; Length 6;
 XX Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 XX Sequence 6 AA;
 XX
 XX QY 1 FLFSWY 6
 XX Db 1 FLFSWY 6
 XX
 XX Query Match 68.1%; Score 32; DB 6; Length 6;
 XX Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 XX Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX Sequence 6 AA;
 XX
 XX RESULT 15
 XX ABR45524 standard; peptide; 6 AA.
 XX
 XX AC ABR45524
 XX AC
 XX DT 10-JUN-2003 (first entry)
 XX
 XX Staphylococcus aureus CHIPS-related peptide #714.
 XX
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 XX formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 XX inflammation; cardiovascular disease; central nervous system disease;
 XX gastrointestinal disease; skin disease; genitourinary disease;
 XX joint disease; respiratory disease; HIV infection; antiinflammatory;
 XX cardiant; cerebroprotective; nootropic; dermatological;
 XX synecological; immunosuppressive; anti-HIV.
 XX
 XX OS Staphylococcus aureus.
 XX OS Synthetic.
 XX
 XX WO2003006048-A1.

XX
 PD 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-de Haas CJC, Kruijzer JAW;
 PI Van Strijp JAG;
 XX DR 2003-256333/25.
 PT Combination of peptides derived from chemotaxis inhibiting protein from
 PT *Staphylococcus aureus* (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure: Page 13; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR4811-ABR47162 and ABR47164
 CC -ABR4735) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC *Staphylococcus aureus*. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC disease, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection.
 XX
 SQ Sequence 6 AA;
 Query Match 68.1%; Score 32; DB 6; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLFSWY 6
 DB 1 FIFSWF 6

Search completed: March 18, 2004, 13:35:08
 Job time : 54 secs